

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGT**CATG**GCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGTTGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTTGGTCTGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTTCAAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGT**GTA**ACCCAATGTATCTGTGGGCCTATTCCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

1005610-12101

**FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902

><subunit 1 of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLINEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPKSCCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT  
GTTCCCTCTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGCCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACCTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGACACACT  
GGCAGTAATACGGACTCTTGTAGATAAGTAAATATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

100550.4201  
102121.0251001



GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTTCAGCCCATTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGACTG  
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAAA

**FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT  
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT  
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACCTAAAGATTGAAG  
ACATCACTGATAAGTACATTTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC  
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
CTGATCAATAATGCTGGTGTTCGCGCGTGTGCTGGCTCCCCTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCA  
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAACAA  
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG  
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG  
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT  
AAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGPHVIAACLT  
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGKGLWGLINNAGVPGVLAPTDW  
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF  
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEgyIEKSLD  
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK  
AELANPKAV

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCC**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCCGTGCGCCACCACT  
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCGGCGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAAACCAGCAAATCCACCCGTCTTACCAG  
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTTCGTACAGAAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCGTGTGGATCCCCGCCCGGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGTCATCTGAACATATCGCCAGAAGGGCGTGATTGACGTCTTCTGCATGCATGGA  
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
 GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGGACG  
 TGGACGTCAACCTGTTTGGAGGACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC  
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG  
 TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCCGCCAGCCACATGGAGCTGGCCCAGGA  
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
 TGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA  
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACAGGGTCC  
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCCGAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCCTCTGCCTATCT  
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCAGGCT  
 CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
 GGCCGTCACTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCTC  
 CAGAAGACACGAATCATGACTACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGCAGC  
 TCTGCCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC  
 CTGGCCGCCCCGAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCT  
 CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTGCTCTAACCGCAA

**FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTTPVVGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN  
 SKSWRRRSCWRKWKQLSRLQQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE  
 IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT  
 KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY  
 RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA  
 RKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
 PYSDVNIGTGVAHPPRWTS DSTVAEVT SIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK  
 KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
 HLLRHSEPSKLT FVGELAHGRFS AKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
 MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHLLRPETVESLFYLYRVTGDRKYQDWG  
 WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD  
 AYVFNTAEAHPLPIWTPA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
CGCCTCTCCGCACG**ATG**TTCCTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACCAACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
GCCCCTCGGGAATCACAACTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGG  
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCC  
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
GGACCCCCCTGCCTTCCTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC  
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR  
GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFERFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



CAATGTTTTGCCTATCCACCTCCCCCAAGCCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATTAAGAAATTGTTCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:****Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAG  
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG  
 GCCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
 CTCGCCCCGCAGGCCCGGCCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGGCCGCGCGCA  
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG  
 GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC  
 AGGGCGGCGGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTT  
 GCCCCAGATACTCTGCCCAACCGCACGGTCACCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAATCTGGTTC  
 GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG  
 TCATTACGGTCTTTGGAATTCCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT  
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
 CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT  
 GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT  
 TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTTGTGGTATCAGGATG  
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC  
 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTG  
 GGGCTGTCATGTCCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
 AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGGCAGATGATGATTATTCTCGCTGTGAGTATGCAATGATGTCACTAGAGTTCTTTAT  
 ATGTTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACCTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTATTCAACATATTACCCAATATTGCTCTGGAAGCTTATGTATCAAGTCT  
 ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTTCCGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT  
 GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
 AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
 AAAGATTTTTTTTTGCGAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT  
 CTTACATAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAATATACT  
 ATTGTTACATGTGAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTGCTCCT  
 GATTTTAAGACAATAAGATGTTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC  
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAATCAAGCAAGCTGTAT  
 ATCAAAATTTTTGGCAGAAAAACAAATATGTCATATATCTTTTTTTAAAAAAGTATTTCA  
 TTGAAGCAAGCAAAATGAAAGCATTTTTACTGATTTTTAAAATTGGTGCTTTTAGATATATTT  
 GACTACACTGTATTGAAGCAAAATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACCACATT  
 TTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG  
 TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAATGGC  
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRGRGAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPDTPNRTVTILISNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT  
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPEVVNNKGDFRWPRTL  
LAGITAYLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQ  
MPLNL TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGFRFTKEEKS  
KELGDVMVDIASNIMLA DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIA  
LEAYVIKSTGFTGMTCT VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSN  
TFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560

**FIGURE 17**

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA  
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGGAGAGACGCTCCTGATCGTCGAATCC

## **FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

10035610.121201  
"02121" 01251001

**FIGURE 19**

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTGCTTCTCCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCCACCAC  
 CTATGTCCAGTTCCTGTCCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCGGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCCTGTCGGGGCTGGCCTTGCTGTC  
 TGTCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTCTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCCACCTGGTTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCCTTTCTCTGTTTTCTCTTCTGTCTCCCCTCCCTCCCACCTTTTTCTTTCTTCC  
 CAATTCCTTGCACTCTAACCAGTTCCTGGATGCATCTTCTTCCCTTTCTCTTGTCTGT  
 TTCCTTCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCTGTCGGCTTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCTCCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCTTGACGCCGTCCATGCCACAGCCCC  
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT  
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT  
 ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG  
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT  
 CTGTGGTATGAAAAAG

**FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPTFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAI AATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI  
IFAFISDPNLYQHQP ALEWCVAVYAICFILAAIAILLNLGECTNVLPIPFPSFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFVKV

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21



[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSP LSSLAQVNLS PF SHPKVHMDPNYCHPSTSLHLC S  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALES AFSSY  
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQT VSPDTLCSSLC SLEDGLLGSPARLASQLLGDE  
LLLA KLPPSRESAFRSLGPLEAQDSL YNSPLTESCLSPAEEEE PAPCKDCQPLCPPLTG SWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT  
GGCACCTCCTGCTCAGTGCAGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCCTTTCAGACAGGACAACCTGTGATATTTAGTTCCCTGATTGTAAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACA**ATG**TTGGCCTTAGCCAAAATCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA  
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTCACCAATAATTCAAAACTCTTTCCAA  
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAAAGGAAAAC  
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCCTATGGATGACATACC  
TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTCTA  
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

**FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKT MENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSEFVSKVPWNA  
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLTVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA  
MPPESEENARDGIPMDDIPPLRTSV

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

**FIGURE 25**

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTTGATTCTGAGGATCCTGCA  
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG  
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACCTGC  
 TATCTGATGCCCCCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGTCCTTGGAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
 AAAAAAAGGAAAAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAA  
 TGGCATTGCTTGTTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG  
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC  
 GTTGTTTTTTTTGTTTGTTTGTTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTTGAACTTTTTGTGTAAAATATA  
 TCAGATCTCAACATTGTTGGTTTCTTTTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA  
 AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG  
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA  
 CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

**FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF  
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPPLNTSIVMPPKNLVELFGKLASG  
RYLPQTYVVREDLVAVEEIRDVSNLGIFITYQLCNNRKSFRLRRDLLLGFNKRAIDKCWKIR  
HFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCCAGTCCTGTACGCC  
 AAGGAACTGGTCCTGGGGGCACCATGGTTTCGGCGGCAGCCCCCAGCCTCCTCATCCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCTTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG  
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCGCGGGGGCCCCCGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCCCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
 GGGACATGGGGTCCCAGTGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG  
 GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCCTGTGCTTGCAGCAGTGTCCACCCCAG  
 TGTCTAAAGTCTCTCCCGGGCTGCCAGCCCTGACTGTTCGGGCCCCCAAGTGGTCACCTCCCC  
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
 GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA  
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGGAACCTCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
 TGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCCTGCTTTAGGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA  
 AAAGA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAAATQNLKSP  
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248



**FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
 GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG  
 GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAG**ATG**  
 AAGTTCCAGGGGGCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG  
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC  
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGGCAGCT  
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
 GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG  
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA  
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG  
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG  
 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT  
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC  
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT  
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC  
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG  
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG  
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGA  
 TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACCC  
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTGAGGGCTTCA  
 GAGGACAGGGAGTTTCCAGCAACATGAGGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGGA  
 GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT  
 TGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT  
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA  
 AGCTCTCGCATCCCC**TGA**CCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACT  
 CCCTCCTTAAAACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTA  
 GCTGCCCCACAA  
 AA

**FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA  
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM  
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS  
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW  
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL  
GGSGDNRYRGQSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ  
RSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG  
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA  
 CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGCGAGGAGAGTGAGGGGAAG**ATG**TGTTTCTTGAACAAGC  
 TGCTGCTACTTGCTGTCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTTCTTTCTGGAAGAGG  
 GTCCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGGACCAGC  
 AGCTGCTCTACACCTGCTGCCCCCTACATCGGAGAGCTCCGAAACTGCTCGCTTCGTGGGTGTCAGGCAGTAGTG  
 GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTTCCCAGACCA  
 GCCAGGGGCTGCAGGCACAGCTCGCCCAGGCCTTTTCCACAACCAGCCGCCCTCCTTGCGCCGACCGTAGAGT  
 TCGTGGCAGAAAAGAAATTTGGATCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG  
 CAGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCCAGCTGTTGGAGATCT  
 TGTGTTCCAGCTGTGCCCTCACGGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGACAGAAATTTGCTGTGGGGC  
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCGCACACTTCGAGCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCC**TGAC**  
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCTGACGAGGAGTCTCCCAGAGCATCTGGAACAGCTCCTTAGGC  
 CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG  
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG  
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCCTTGTGGAAGGAAGACTTTCAGGGGCCGGTTCCGCTGCAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA  
 CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCTGCCTGGGCAGCCTCCACCAGGCCAG  
 TGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC  
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCCAGAGCTAGGGCTGAGAAGTGGCC  
 CTGCCCTTGGGCATTGCACCAGAACCCTGGACCCCCCGCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCCTCAC  
 TGTTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCCTGGCATCCACCACGCCGA  
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCCCTGGAGTAGAA  
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAAGCCT  
 CATTTGCTATCCCAGCATCTCTTAAACCTTTGTAGTCTTGGAATTCATGACAGAGGCAAATGACTCCTGCTTAAC  
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCCCTGAGGTGCGCG  
 GACTGCCTGAGGTGAGGAATTCAGAGCCAGCCTGGCCAACATGGCAAACCCCATCTCTACTAAAAATAAAAAAA  
 TTATTAGCTGGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC  
 CTGGAGGTGGAGTTGCAGTGAGCCGAGGTGCGACCACTGCCTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG  
 AAAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCCCTG  
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTTTTAGAATAAA  
 CTGGTTTTTCTTTAAAAAAGGGCTTTTATTAATAATCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC  
 TGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG  
 GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTCCGGGCACAGAGCTGCGGGGTCTGGGGGACCCGGG  
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG  
 GGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGCCGGTGTCTCTTCTAGGCCAGTCCCTGGGGAACTAAGCTC  
 GGGCCCTTCTTTGCAAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGT  
 GAAGAGGGCGCCGGTTTGTGGCTGCAGCGGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTCCGTCTA  
 ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGGCCTCAGGAAGTGGCCTTGGACGAGCGTCAT  
 GTTATTTTCACAACTGTCTGCGACGTTGGCCTGGGCACGTCATGGAATGGCCCATGTCCCTCTGCTGCGTGGAC  
 GTCGCGGTGCGGGAGTGCGCAGCCAGAGGCGGGGCCAGACGTGCGCCTGGGGGTGAGGGGAGGCGCCCCGGGAGGG  
 CCTCACAGGAAGTTGGGCTCCCGCACCACCAGGCAGGGCGGGCTCCCGCCGCCGCCGCCGCCACCACCGTCCAGG  
 GGCCGGTAGACAAAGTGAAGTTCGCGCTTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGGCGCAGCGCG  
 TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGGCGCT

**FIGURE 32**

MCFLNKL L L L L L L A V L G W L F Q I P T V P E D L F F L E E G P S Y A F E V D T V A P E H G L D N A P V V D Q Q L L Y T C  
C P Y I G E L R K L L A S W V S G S S G R S G G F M R K I T P T T T T S L G A Q P S Q T S Q G L Q A Q L A Q A F F H N Q P P  
S L R R T V E F V A E R I G S N C V K H I K A T L V A D L V R Q A E S L L Q E Q L V T Q G E E G G D P A Q L L E I L C S Q L  
C P H G A Q A L A L G R E F C Q R K S P G A V R A L L P E E T P A A V L S S A E N I A V G L A T E K A C A W L S A N I T A L  
I R R E V K A A V S R T L R A Q G P E P A A R G E R R G C S R A

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

**FIGURE 33**

TCCCTTGACAGGTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC  
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**  
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGGCTCCCTGCGGGGCCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAAAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTCAGCAGCTCCAGCCACCTGCT  
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCATTC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
 CATCTTCTGGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG  
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT  
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG  
 GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGGCCCCGCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTTCATCACCCGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA  
 TCACCTTCTCCCACCCCTCCTGGACC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCTAG  
 AGGAGAAGCAGCCTCCGCCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTTG  
 CCCCCTCAATTTCCAGCACCCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG  
 CACCCTTCTGCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCTTTCCACCTCCCCTACAA  
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCCTCCCAGCCACTATCCCTTGCTGGAAGGCT  
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTC  
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT  
 CTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT  
 ATCACTGGGTCTGTCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG  
 GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAATGATTTGTACAGGAATAAACACACCTACGC  
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 34**

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELCHVHVYGMVPPNYCSQRPRLQRMPIH  
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

GTTCTCATAGTGTGGCGCTCTCTAAAGGAAAAAACACTAAAATGAGGAACCTCAGCGGACCGGGGAGCGACGCAGCTT  
 GAGGGAAGCATCCCTAGCTGTGTGGCGCAGAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCAGAGGTGTCTGAGGGGCTGG  
 GCGCAAGGTTGAAAGAGTTTTCAGAAACAAGCTTCTTGGAAACCCATGACCCATGAAGTCTTGTGCACATTTATACCGT  
 CTCGAGGTTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTTCGCCAGGAGCGGCAGATATCTCTTTGTGTGACCTTGGC  
 GGCCTATGGGACGTTGGCTTCAGACCTTTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
 AGGCCTGAGGTACACTGGCTTGCTCTCTAGCCACGAGGCTGCTTTGTGACTTGAACGAGGTCCCTCAG  
 GTCACCGTCCAGCCTGCTCCACCGTCCAGAAAGCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA  
 AGGATGAATGTAACCTGGCGCTGAATGGAAGAGACTGAATGGTCGGATGATGCTCTGGGTGCTCTCATCAC  
 CAGGGGACCTTCGTTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCTGCG  
 GGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGT  
 ATTGAAGTGGATGAGGGAACACAGCAGTTCATTGCCCTGCCACTGCTGAGAGCACCACCCCAAGGCCAGGTCCGG  
 TACAGCGTCAAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGACGAGGCTATGACAAGTGTGCAGCTACAACCCAGTGACCCAGGAAGTGAAACCC  
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC  
 CAAACCATCATCGTCACCAAGGCCAGAGTCTATTCTGAGTGTGTGGCCAGTGAATCCCACCCCGAGGCT  
 ACCTGGGCAAGGATGGTCCAGTGTACCGGCTACAACAAGACCGCTTCTGTGAGCAACCTCTCATCTGCAC  
 ACCACCGAGGAGGACTCAGGCACCTACCGTGCATGGCCGACAATGGGTTGGGAGCCCCGGGGCAGCGGT  
 ATCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTTCATCCCTGGGGC  
 CAGAGTGCCAAAGCTTACCTGTGAGGTGCTGGGAACCCCCCGCTCCGTGCTGTGGCTGAGGAATGCTGTGCC  
 CTCTATCTCCAGCGAGCGCTCCGGCTCTCCCGAGGCCCCGCGCTGCTCAGCATGGGCTGAGGACGAAGG  
 GTCCTACAGTGCATGGCCGAGAAGAGGTTGGGAGCGCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC  
 ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAACCTCGGCAAC  
 CCTGAGCAGATGCTGAGGGGCAACCGCGCTCCCGAGACCCCAACGTCACTGGGGCTGCTTCCCCGAAGTGT  
 CCAGGAGAGAAGGGCGAGGGGCTCCCGCGAGGCTCCCATCTCAGTCCGCCCGGCTCCTCCAAGACAGAC  
 TCATATGAATGGTGTGGCGGCTCGGCATGAGGGCAGTGGCGCGCCCAATCCTCTACTATGTGGTGAACAC  
 CGCAAGCAGGTACAAATTTCTCTGACGATTGGACCATCTCTGGCATTCAGCCAACAGCACCCTGACCTC  
 ACCAGCTTGACCCCGGAGCTTGTATGAAGTGGAGTGAGCATTTACAACCTGTGCGGGAGAGGGCCAGACAGCC  
 ATGGTCACCTTCGAACTGGACGGCGGCCAAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC  
 GACCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCAGCGCGCTCTCCCCCAGAAAGCTCCGACAGG  
 CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCCAATC  
 CAGTCTCTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACAGCGCCATCCCCC  
 TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCTACAAGTTTCAGTCCGGCTCTGAACATG  
 TCGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGCTACAGCGGTGCGGTGTACGAGAGG  
 CCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC  
 CCAGCAAGTAAACAACAACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAACATGATAGT  
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTTCATCAGCCACCTGCAGCCAGAGACCTCTAC  
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTACGAACGTGATGATCTGTGAGACCAAAGCT  
 CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGCACCCCCAACCTCTGGCCCCACCACAGCCGCCCTTCTGAAACC  
 ATAGAGCGGGCCGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACTGCCCTATGCTATTGTGGGGTCTGT  
 CTGGGCTCCATCTTCTCATCATCTGTCACCTTCATCCCTTCTGCTTGTGGAGGCTGTGCTAAGCAAAAACAT  
 ACAACAGACCTGGGTTTTCTCGAAGTGGCTTCCACCTCCTGCCGTATACTATGTTGCCATTGGGAGGACTC  
 CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGATGAAGCCCCAGCAGCAGTCCCGAGGCGAGCTTCAG  
 CAGCAGAGTGACACCCAGCAGCTGCTGAGGCAGCCATCTTGGCAATGGATATGACCCCCAAAGTCAACAGAT  
 ACGAGGGTCCCAAGCTAGCCCGGACGAGGGCTCTTTTATACACACTGCCCGAGCACTCCACTCACCAGCTG  
 CTGCAGCCCCATCAGACTGCTGCCAACGCCAGGAGCAGCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC  
 CCGACAGTCTGTCTGGAAGCAGTGTGGACCCCTCAATTCAGTCAGGGCCCCCATGCTGCTGTGGGCTTGTG  
 CCACTTGAAGAGGTGGACAGCTGCTGCTGCCAAGTGGTGGAGGAGCTGGTGTCCCCGACCCCGTAGGG  
 GCTTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCAGCTGGTGGTGTCTTTTGAACACCACCT  
 CTCACAATT**TAGG**CAGAAGCTGATATCCAGAAAGACTATATATTTGTTTTTTTTTAAAAAAGAGAAAAA  
 AGAGACAGAGAAAAATTTGGTATTTATTTTCTATTATAGCCATTTATATATTTATGCACTTGTAATAATGTAT  
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGTTGGAGAGGAAAAATAAGAAAGCTGCCA  
 CTAACAGGAGTCAACCGAGAAAGCACCGCAGGCTGGCGGGACAGACTCTAACCTGGGCGCTCTGCAGTG  
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCAGAGCA  
 TGAGGGAACAGCAAGGGGCACGGTATCACAGCTGGAGACACCCACAGATGGCTGGATCCGGTGTACGGGAA  
 CAATTTTCTAAGATGCCATGAGAACAGACCAAGATGTGTACAGCAGATGAGCATTAAGAAACCTTCCAGAA  
 CATAATTCCTGGCAACATATCTCTGTAAAAACAACACTGTAACTTCTAAATAAGTTTAGTCTTCCCTGTAAA

**FIGURE 36**

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEWDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIITYPPEAQTIIVTKGQSL  
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKGQAPAEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNT  
 PIHGFYIYYRPTDSDNDSYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVM  
 ICETKARKSSGQPGRLPPTLAPPQPPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSIVL  
 IIVTFIPFCLWRAW SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCPSAAVGYPGMKPQQHC PGELQQQSDTSSLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHHCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCC LGLVPVEEVDS PDSCQVSGGDWCPQH PVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879



**FIGURE 37**

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCACGGGCCGCGAGGGTTCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC  
 AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTTGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC  
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTATGACGGGACT  
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT  
 CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
 TGCT**TGA**CACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

**FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELV TSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLR SFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC  
 AAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG  
 TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTT  
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA  
 GGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTCAGCATGTGTTCCCTTTCTGCAGTG  
 GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
 CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC  
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCTGTACTTGGGTGCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA  
 GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG  
 TTTTATTTCTCTCA

**FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM  
PVPBGHDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE  
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

1005630.4204

**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCGACCCAAGTGAGGGGCCCCGTGTTGGGGTCTCCC  
 TCCCTTTGCATTCCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGCGCGCTTGATG  
 CGGAGCAAGGATTTCGTCTGCTGCCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCCAAACTCAACTCCATCAAGTCCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTGGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCCTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA  
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
 TCAAACCATGACTTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA  
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA  
 CCAGTGCTCCATCAGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTCCAGCGT  
 TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGGTGGAAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA  
 AAAGGGAGAAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAAGCACACAGTGGAAAT  
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA  
 TACAATAGGTTCTAAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTTGTTAATTTACAACAGAAAAT  
 TACCTTTTGTATTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTCCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAAACAG  
 CCACAAATACTTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATATCTCTTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTCCA  
 AACTATACCCATAAATTTGACTAGTAAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAATTTAAA  
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT  
 GATAGAATTAGATTGGTAAATACATGTATTCTACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTTCGTTTGTTTCAGGTTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCCGTACTATCCTCAAATTTATTTTATAG  
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
 TTTCAATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA  
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTGAAACCACTTTACTACTTTTTTTAACTT  
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG  
 TAGACCACAATTCATTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG  
 AGATTGAGTTTGAGCCTGTATATCTATTAATAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA  
 CATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGTTTGTATAAACAGGT  
 TGCTATAAGCTTGTGAAATGAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTTATTTACAAT  
 TTGGTTTTCTGCAATATTTTCTTATGTCCACCCTTTTAAAAATTATTTTGAAGTAATTTATTTACAGGAAATG  
 TTAATGAGATGTATTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC  
 TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCCTCTAAAAACTGAAAAA  
 AAAAAAAAAAAAAAAAAA



**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT  
 CCTGGTTTGGAGTCCTTTCCCTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCGTTAAAAAGCAGCCCTTTTGCTTTTTTGT  
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC  
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24

TOP-44-249



**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTCACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG  
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA  
 CGGGCCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG  
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC  
 TGTCTCCTGGCCGCCCCGAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTAACTTGGCGGAGTTGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAAT  
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCTCCT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC  
 AAAATCCCACTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA  
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
 CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGGCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTTAAAAAAAAA  
 AAAAA

**FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRHVEEAQQVVHWDRQPPGVPHDRADRLDL  
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEPFPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPKPKYIDLKDKGRKENCK

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

TOP SECRET

**FIGURE 47**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT  
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT  
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
CGTGTCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTTGTCTGCATGGTGATCC  
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTTCTATG  
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
ATTGGTGGACTTGCGTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG  
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA  
GGACTCCCTCAGTGCCCCCTTCGGTGGCCTCCAGATTCAATTGATTCCACACACCCCCCTCTCC  
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC  
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
GTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACCTTTGCTGACCTAT  
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGG  
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT  
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
CTCAGCCTGCTCTACCCCTCCTGGTGCACCTCATCT**AGA**AAGGGAGGACACAAGGACATTGGTG  
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACT  
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA  
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT  
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
AGTCCCCTGGCATGGTCAGTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
GCGGGTGAACAACTGCCCCTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT  
GCTTCATTCCAGAGGGACAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
GTATTCAAAAA

**FIGURE 48**

MAVVS EDDFQHSSNSTYGT TSSSLRADQEALLEKLLDRPPPG LQRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAI FMVITALVKVD TSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLA AHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITS LIYPAVCTNIESLNKGS GSWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKT VVFQSDVYPALLSSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472

**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA  
 TCTCCACCGAGAGTCA**ATG**GCCCCATTGGCCCTGCACCTCCTCGTCCCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCGAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG  
 CTGCACTACGTGCCGGCCACCAAGGTGTTCCCTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA  
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC  
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTTCGGACGCGGCGGCAGCGTTCGCC  
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTCTGTGCGCCAGCTCTGGGACGGCACCGGCGTCGTCAAGCGTTGGGCGGAGGACCAGCACA  
 GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT  
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGAAAAA  
 AA

**FIGURE 50**

MAPLALHLLVLPILLSLVLASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRI  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLO  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT  
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
GAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCTCT  
GCTGCTGTTACAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCACTTCCGACCCCGGCGTTGATCTGCAT  
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA  
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTTCCAGAAGAACAATGACCTAACAAAGTTGCTG  
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC  
CTGTCTCTTGATAAAAGGTTATAAATCATCACCAGACAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG  
GATCATCTCCGAATTGGCTTGTACACGTAATCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTTGGTGCTGAT  
AGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA  
GCAAAGAGGGGAGAAGAGTGAATGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG  
AAAACCTGTGCCTCCTAGCCCAAGAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG  
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA  
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
CACATTTGTTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCT  
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTTGCTCACTGGAGC  
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTGAGGTGTATGAAGCTTATGGTCA  
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACGTTGGGGTGCCCTGGC  
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAAGTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGTGCTG  
GCTTACACAGGAGACATTGGTTCGCTGGCTCCCGAATGGAAGTCTGAAGATCATCGACCGTAAAAAGAACATTTT  
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAAGTGTAC  
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCTC  
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
AGAAGACTTGAGAAAATTTGGGAAAGAAAGTGGCCTTAAAACCTTTTGAACAGGTCAAAGCCATTTTCTTCATCC  
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG  
TGCACTGCTTGTGAGAAAATGGATTAAAAAATTTTACATTTGTTTTGCCTTTCTCCTATTTTTTTTTTAACC  
TGTTAAACTCTAAAGCCATAGCTTTTGTATTTATATTGAGACATATAATGTGTAACTTAGTTCCCAATAAATCA  
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
GATCCAGTTTATGTTCTGTGCTCCTTCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
CAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTTGTGATAAACATAAAGTGGCAACAGTCTCTATGCTTATTTACA  
TCTTCTACTGTTCAAACATAAGAGATTTTTAAATTTCTGAAAACTGCTTACAATTATGTTTTCTAGCCACTCCAC  
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
CTGCGTAAATTAATTTGTGTACTGAAGGGAAAAGTTTGATCATACCAACATTTCTTAACTCTCTAGTTAGATA  
TCTGACTTGGGAGTATTAATAATTTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
CAGTAGGAACTGGGGAGTAAATCTGTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
GGTGGGCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAAGTGGGAACAAAGATCT  
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCCTTGAT  
AGAGTTCTGTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATTAAC  
TATTACAGATAAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN  
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
PDQFVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPSPED  
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLLKCEHAYEPTPDDVAISYLPLAHMFERIVQ  
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
SQPVLQIFVHGESLRSSSLGVVVPDTPDLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI  
GKESGLKTFEQVKAIFLHPEPFESIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622



**FIGURE 53**

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG  
 CCCGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGGT**ATG**GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGGCCGTGCTTTTCCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCCCTGGACGTAGA  
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG  
 AGGCCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCCT  
 CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTCTTCCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCAATTGCAG  
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT  
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG  
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTCACGAGGCC  
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGGAAGTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTCTGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCCTGGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC  
 ACCCCAATTTTCCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
**ATGA**GACCTCCTCCAGGACCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA  
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCCTGCTCCAACACCCCGTTCTGAGTT  
 AAAAGTCTATTTATTTACTTCCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA  
 ACCTATTTATTTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCCTGGATTTT  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA  
 GACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT  
 GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVIVNIKLILDTR  
 RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
 REQGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK  
 DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS  
 AEEAECHWADTELNRNRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
 RPNLYLRMLRSLLSAQGVSPQMITVFIDGYEEPMDVVALFGLRGIQHTPISIKNARVSQHY  
 KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
 EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS  
 RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKLKEAYEVEVHRLLEAEVLDHS  
 KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVIRGNHRGLWRLFRKKNH  
 FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGAACACCACAC  
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCCACTGGAAATTTGTTGTCTAGTGGTTGTGGTGAATA  
 AAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGCTTTTGG  
 GTGCTGGCCTTCTCTGTGGAACCTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA  
 GATATTTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCCTCCCTGAGGTGGGCGGA  
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT  
 GGTTCTGGGTTGCCTCATCCCTCTCATCTGTGCTAGTAGGACACCAGCATTAATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC  
 TCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTTAAAACCTG  
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT  
 TATCTTTTAAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCTATTCTCAGGGAAGATG  
 GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT  
 AACATGGTTCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGTGCATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT  
 TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAAT  
 ACCTGTCTCCACATTCCCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCTCCTTCAAGAA  
 CAGTCAGATCACAAAGTGTCTTTGGAATTAAGGGATATTAATTTTAAAGTATTTTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTTTAAAAGACTACCAAATGTATGGTTGTCCTTTTTTTTTGTTTTT  
 TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAAGCTTT  
 GCGGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCGCTA  
 TTGATTTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTTCTTTGCTTTTCTTCTAATCTT  
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATT  
 CTTATCAGGACAACCACTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATTCTTTATCCCCTT  
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAAATACCACCTCCTCATGTGTAA  
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA  
 ATTTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTAT  
 TATTAATTTATTTTTACTTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG  
 ATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA  
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACTATATGGTTGCCTAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILLSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

1005640-1204

**FIGURE 57**

GCTCGAGGCCGGCGGCGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAG**ATG**ATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA  
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA  
 TAACATCACCCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAA  
 GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
 CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTC**TGA**ATTGAACTGGAATCACATATTTCAACAGGGCCGAAGAGATGACTA  
 TAAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

**FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

**FIGURE 59**

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGCTGCTTCTTCTACGCTGGCATTGCCCTCTTCA  
CCAGTGGCTTCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTGTGTTGGTGTGA  
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT  
TCCTGGGCAAACCTAAGCTCCTTGCAGAGGATCCTGGAGATTACAGCCCCACCATGCCCGCTCTACCGATCTCAGG  
TTGACCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG  
GTAGTAACCTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG  
TCTTCATGGGAGATGATACCTGGAAAGACCTTTCCCTGGTGTCTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA  
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG  
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA  
AGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC  
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACCAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC  
CCACGCTGGCCCTGCTGCTGGGCCTGCCCATCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG  
GGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT  
CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
TCTCCAAGGCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA  
TTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTGCTGCC  
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC  
CAGGCTTTCCATTTGCCCCCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC  
TCTTGGGAACATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT  
TTCTGTGGAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCGTCC  
TGTTACTCCTGCTGTTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT  
TCCTTTTGGGCTCATTATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC  
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG  
GAATTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTTCACTGTTGCCCTGAAGAGACACCTGTTTGGCACT  
CCTTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAGAATTTATGGTATGGAGCTTGTGTGG  
CGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGGTAATCTCAAGAGCCCCGAGCCAC  
CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTCGGGGG  
CAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCTGGGGCATCCATGGTGTGCTCGGGCTGTAGCAGGGC  
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA  
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA  
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAAATCTCAGGGTCCCCTGACTGTGGCTG  
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCCCTTCTGCTGT  
TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCCTACATCTGCTTGTG  
CTGGGATACCCGTCACCACCCTGGTCTTTTACTGTGCCATGGCAGGAGTCTCGGCTTGGGCCCTCATGGCCA  
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC  
CAGAGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCCTCCCACCTCCTCT  
TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC  
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG  
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTTCAGATT  
TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGCAGGCATCTCATGGTCTGGAAGTGT'TTGCCCTAAGTTTCATAT  
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG  
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT  
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTAGGACCACAGTGGAGTA  
TGATCCCTAACTCCTGATTTGGATGCATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGG  
GCGTGGTGACTTGCACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA  
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAAGTGAATAAAATGATAATAT

**FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW  
 MASRFSRVVLVLIDALRFDFQAQPQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ  
 VDPPTTTMQRLKALTGTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLF  
 PGAFSKAFFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGHHPHEM  
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST  
 PPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ  
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
 ARAMCIESWARFSLVRMAGGTALLAASCFICLLASQWAI SPGFPCPLLLTPVAWGLVGAIA  
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLLFRLA  
 VFFSDSFVVAEARATPFLGSGFILLLVVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY  
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA  
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAWALASGADEAPPRLRVLVSGASMVLV  
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
 EFRGRLERTKSQGPLTVAAYQLGVSYSAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
 LLHLLAAGIPVTTGPGFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS  
 CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEEP  
 LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWVKVFAPKFIFEAVG  
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
 1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271



**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT  
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTTCCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA  
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGAT  
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCACTGACATTTGTGCGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG  
 CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC  
 AACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC  
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
 TGTTCATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG  
 TGGGTGT

**FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISSVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFD  
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL  
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
 TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
 GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCCAGATCATCGGGGGCCACGAGG  
 TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACTGCGGA  
 GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCCACTGCTTCAGCCACAGAGACCT  
 CCGCACTGGCCTGGTGGTGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG  
 TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC  
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
 GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
 TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
 TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA  
 ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC  
 GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC  
 CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
 TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
 AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
 AAGGGCAGAAGCAAACCCAGTAAATGTTAAC TGACAAAAAAAAAAAAAAAAAAAAAGAAA

## FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
```

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRPLPGRRARPPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLLTLMCTRSGDSHRRGFC SADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**

amino acids 1-30

**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG  
 CAGGCGCCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTCGCCATCGTCCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCAGCCCAGCACATACTGGCCGTGGCGGAGGAACTGGCGGATGTT  
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCCTCCCCAGAT**TAA**CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGGCTGAGGGCTTCCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC  
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACAGCTGCTGCTACAGGACCTGGGA  
 TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAAC  
 TTGCTCATTT

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN  
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSP ELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW  
AESARLVGLEAPSVREQPLPR

**Signal peptide:**

amino acids 1-17

10015610:12301  
10015610:12301

**FIGURE 67**

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCA  
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCACGTGGTAGC  
 TGAGGCTGTCAATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTGAGACCCCTGGGTTCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCTCTAT  
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA  
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCCTGTCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC  
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG  
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC  
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
 ATGTTTATAAATCAAAA

**FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGWKTEDASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPLHQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19



**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
 CGCCAGG**ATG**CCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT  
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC  
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
 ACTTCCTGAACGACAACATTTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA  
 CCTGCTGCATCAGGAACACGACAGAAAGTTGTCAACACCATGTGTGGCTACAAAACCTATCGAC  
 AAGGAGCGTTTTAGTGTCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTCATGGACAACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCCAAT**TAG**GGCCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGGCCCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA  
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTCGCCCTCGGGGCAGGAGGGAAGG  
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC  
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA  
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
 TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTTAA  
 TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL  
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGVPYTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV IWFMDNYTIMACILLGILLPQFLG  
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAG**ATG**GCCGGCCCGTGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC  
 TTGATCCAAGCCACCCTCAGTCCCAGTTCATCCTCGGCCCAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
 GTCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAAGTGTGATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC  
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT  
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG  
 ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTCCTCCA  
 GTGAAGCCCTCCGCCCTTTGTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAG**TGA**AGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAAACACTTGCCTGTGAAAAA

**FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM  
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITIQLYL  
GAKLLDSQGVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAABAVALSPPEEFMVLLDSVL  
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL  
RPLFTLGLIEASSEAQFYTKGDQLILNLNINSSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL  
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

**FIGURE 73**

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAAGTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
 AACTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTTGCCATGGTGGATTTTG  
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT  
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTGCAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
 GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGTCTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGT**TAAAA**AGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAAGAAGATGCAACTTGTATATTTTGTATTAC  
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAAATAATTATCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA  
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATG  
 GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCCCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA  
 GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAATA  
 TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
 TTGTCACCTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAATCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

**FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRNPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLA VIGGLVYLRRSNMEFLFNKTGWAF AALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFN GGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

100561012001

**FIGURE 75**

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA  
 GAACGCCAGAGGGAGGCGGCTGGCCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCGGATGCTA  
 CTGCTGTGGGTGTTCGGTGGTCGCAGCCTTGGCGCTGGCGGTACTGGCCCCCGGAGCAGGGGA  
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTTCGTGAGCGACTCCTTCGATG  
 GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTTATGAAG  
 ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC  
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAAGGGTCTAG  
 ATCCAAATTATACAAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT  
 GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG  
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA  
 CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA  
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC  
 TTACCCTTCACCATCTTCTGGAGAAAATTTTGGATCTTCAACATTTACACATCTCTTTATT  
 GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAGAAATG  
 CACCCTGTAGATTATTACTCTTCTTATACAAAAACTGCACTGGAAGATTTACAAAAAAGA  
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG  
 AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACCTATTGTCATATACTCCTCA  
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG  
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAATG  
 TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG  
 AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAAGT  
 CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA  
 CCTACATGCTTCGAACTAACCCTGGAAATATATAGCCTATTTCGGATGGTGCATCAATATTG  
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCC  
 AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG  
 CTTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT  
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA  
 TGAAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA  
 GTTTAAAAATAGTGTTCTAGAGATACATATAAAATATATTACAAGATCATAATTATGTATTTT  
 AAATGAAACAGTTTTAATAATTACCAAGTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC  
 CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC  
 CAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA  
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG  
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTTCGC  
 AAAAAAATAAAAAATAAATAAATAAATTACCAATTTTTTCATTATTTTGTAAAGATGTAGTG  
 TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAATGTTTATTATTTA  
 GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAATACTGTA  
 ACAGTTATGTTCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAT  
 AGTTGTATGTGAGCATTTGATGGTGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFDGRLTFHPGSQVVKLPIFINF  
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS  
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVY  
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSVDIYPTMLDIAGIPL  
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97



**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCATTCCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG  
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

10045610-24301  
T02F01-015Y001

**FIGURE 79**

GCAC TGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCC CAGAATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG  
TGAAGCTGAAGGTT CAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCC**TGA**GAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA



## FIGURE 81

CTCCACTGCAACCACCCAGAGGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTTTGGCAGTGCTGCCCTTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA  
CTCAGCCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGACTCTGAACCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCCCAAGGCTGGCTGGGGAACCCTTCACCCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTTATAAATGAAAA

## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

10056101220102210251001

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCCGCCGCTCCCCGGCACCAGAAGTTCCTCT  
 GCGCGTCCGACGGCGAC**ATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC  
 CACGCCGTATTCCCTGTATGTCTGTCCCAGAGGGCAGAACGTACCCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCCGTGCCCAGGAGCTGGTGC GGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTTGAAGCCTCACACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCCCTG  
 TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTTCGGAGCCCAGCAC  
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
 CTCCAAACTTTGAGGTCATC**TAG**CCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCGTGTTCCAAGGATTTTGGGGTGCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC  
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTAAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAACTACATGGGGAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

## FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
```

```
><subunit 1 of 1, 311 aa, 1 stop
```

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAFVKVATPYSLYVCPEGQNVTLTCRLLGPVDK  
GHDVTFYKTYWRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLTLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVVPSSSQ  
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216



## FIGURE 85

CCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCTCT  
TTCCCCGCGTTTCTCTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC  
TTTCTCTGCCACCGCTGCTTCCTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG  
GGTCTGTGGGTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGA  
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGG**ATG**GTTCCCAGAGTGAGGGTCTCTC  
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT  
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG  
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCCACCAAAGTCCTGCC  
AGCACAAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC  
CGCCTGCCCAACCAGTGTGTCTCTGTCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCACAG  
CCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
GCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
AAGACGTA CTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG  
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
ACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA  
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCT  
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG  
AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCTGGAGCTGAAGGTCACGGCCAGTCCAGA  
CAAAGTGACCAAGACATAACAAAGACCT**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT  
ATTATATATTATAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPEKVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

10045610:121201



88/249

## **FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18

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**FIGURE 89**

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCCTCGGGCTTGAGGGGAAGA  
 GGCTGACTGTACGTTCTTCTACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGCCCAGCACC  
 CCTCTCCTCATCTTGTTCCTTTTGTTCATGGTTCGGGACCCCTCCAAGGACAGCAGCACCACCT  
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCCAGTGCCAGGACC  
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG  
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGA  
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGTAGAGT  
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTAC  
 GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG  
 ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG  
 TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT  
 GCCATGGCTGCCCCGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCA  
 GCTGGTATATGGTGGCTTTCTTTATTTTGTCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG  
 GTGAGATGGAGAACACTTTGCAGCTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGAC  
 AGCTCAGTATTTCCAGCAGAGGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT  
 CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC  
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA  
 TGTCCCAGAGAGAATGCTGAGGCTGCCTTTGTTCATCTGTGGGACCCCTCTATGTCGTCTATAA  
 CACCCGTCTTGCCAGTCGGGCCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC  
 CTGAACGGGCAGCACTCCCTTATTTTCCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT  
 AACCCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA  
 GATGAGGAAGAAAGAGGAGGAGGTT**TG**AGGAGCTAGCCTTGTTTTTGCATCTTTCTCACTC  
 CCATACATTTATATTATATCCCCACTAAATTTCTTGTTCCCTCATTCTTCAAATGTGGGCCAG  
 TTGTGGCTCAAATCCTCTATATTTTGTAGCCAATGGCAATCAAATTCTTTCAGCTCCTTTGTT  
 TCATACGGAACCTCCAGATCCTGAGTAATCCTTTTAGAGCCCGAAGAGTCAAAACCCTCAATG  
 TTCCCTCCTGCTCTCCTGCCCCATGTCAACAAATTTAGGCTAAGGATGCCCCAGACCCAGG  
 GCTCTAACCTTGTATGCGGGCAGGCCCAGGGAGCAGGCAGCAGTGTCTTCCCCTCAGAGTG  
 ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTCTGTCCTCTCTTCCCTCACTCCTCCCT  
 TCAGTGTCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCATTAAA  
 AGGAAAATCCACAA  
 AAAAAAAAAAAAAAAAAAAAAA

## FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
```

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQQHHLVEYMERRLAALERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDGCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVVPFPWVG TGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTQ  
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCT  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 AAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTGAGTCCGCGGTGGTTCCCCCGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCTGACTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC  
 ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTTATTATATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAEILDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
PDHGYWVLRLNGEHL YFTLNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATT PFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255



**FIGURE 93**

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCCGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG  
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG  
 GACGCGTCGCCGGGCCCCGGGTGCGGGGCGAGCCCAGCCACCCCTTCCCTAGGGCGACGGC  
 TCCCACGGCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC  
 ACCACCTTTCAGGCGCCGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC  
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCGG  
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCC  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
 TTCGCCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
 TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATAACCGTGCAACAGGTAAGCAACAGAGGGTGGAAGTGAAGTTTATT  
 TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTTACTTTATATGT  
 TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAG  
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTATGGGAAAAAATTATTGAAGAAT  
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
 ATGTTTATTAATATAACATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA  
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA  
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAG  
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTATTCTTTGACCT  
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAAT  
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC  
 CACTTACGAGCTGTGTTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTTCTTCTCAAG  
 GTTGTGTTGTAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGGTTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA  
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
 GCACTCCAGCCTGGTGAGAGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRSLSLGGGLALLCCAAAAA AVASAASAGNV TGGGGAAGQVDASPGPGLRGEP SHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDL PSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTCACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATTC  
CACAGCA

MGGLLLAAFLALVSVPRQAQVWLGRDLDEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAII FTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

amino acids 1-20

**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCACAGAC**ATG**CTGCTGCTGCTGCTGCC  
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
GCACCCTGGAGTCCGGCTGCCCCACAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
CCGCCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
ATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG  
GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG  
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT  
CTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
TCTGCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
ACAGAT**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA  
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA



## FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTCCCTG  
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTTCACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG  
CAGCCCCCGGGTCTGCACCTCCAGAGCCACCCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

**FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL

EATFTFMREDRCIQKKILMRKTEEPGKY SAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH

MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:****Signal peptide:**

amino acids 1-17

10015610-121201



**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
CCCACCACAGCCCATCACCCCTCATTTCCTACTTGGTGTTCCTGTTCACTCTGTAAAT  
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW  
 AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITITIEHQKCEAYPGNITDTM  
 VCASVQEGGKDSQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCCTTGGTGTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCCTATGAGAAGATATTTTGA  
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

103/249

**FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDIFKKNDDHGDGDFISPKKEYNVYQHDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

**FIGURE 105**

CAGAA**ATG**CAGGGACCATTTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

100561043204

**FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLETFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

1004510-12104  
total 0.5104

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGGCAC  
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCGTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC  
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**  
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGTCCTGGGAACCTTCTTGGAACCTT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

## **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

10045610123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100



### FIGURE 109

CGCGGCCACACGACGCTAGCCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTTGA  
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTTTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGGAATCC  
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTCCTTGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGGCTTCGGAGGCAGAAGTGAGGCCTG  
GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN  
NEGEIDLMSLKRMMKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM  
MFEGKANESSPKPVGPPPERDIASLP

10036610 121201  
root of root

**FIGURE 111A**

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCACACC**ATG**GGCCCCGGGTGGGCAGGGGTGCGCGCCGCGCGTGC

CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTGCGCTGCCC  
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTTC  
CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAACACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT  
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT  
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCCAGCCCCCCTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTTGCCA  
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCCTGTATGGGAACA  
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTTAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT  
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGCGCCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAAGTTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTTCCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG  
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC  
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT  
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCTC  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGTGAGGTGCATCCCCGTCCACGCCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCCCTGAAGG  
CTCCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTC  
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
 AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTGAGCATG  
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTTCAGCTGCGAGTGTGTCCCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG  
 AACACCCCCCACCCTATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC  
 GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCCG  
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACTGG  
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGGCCACGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG  
 GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG  
 ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
 GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCCTGCACCGT  
 GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG  
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT  
 GTGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG  
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTT  
**CTAA**GGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
 ATGTGGGACCCCTGGTGATTTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
 AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAA  
 AAAAAA

**FIGURE 112**

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLKNKLQVL  
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL  
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNOISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIKGLFAPLQSIQTLHL  
 AQNPFFVCDCHLKWLDYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIRSRFS  
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
 SNTDFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRR  
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR  
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNM SHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVEG SFNDLTSLSHLALGTNPLHDCSLRWL  
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGKDCTVPINTC IQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR  
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL  
 DKGFSCECVPGYSGLK CETDND DCVAHKCRHGAQCVD TINGYTCTCPQGFS GPFC EHPPPMV  
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS  
 VELVTNLNQLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTCCTTCCGCA  
GACTCAACTGAGAAATCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGA AAAAAGGCTGTGAGGTTTCCTTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA  
TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

MKAAGILTIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

0000	0000
0001	0001
0002	0002
0003	0003
0004	0004
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**FIGURE 115**

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAAACCTGTACATGGCTCCC  
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG  
 CTTTGACTCAGTTGTTCCCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC  
 CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGAGT  
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCATTCTCAGAAGCA  
 ATAGAAAAGTTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTA**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT  
 CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC  
 CATAGCGAGAGTGCTCTGTATTTTTTTTTAAGATAATTTGTATTTTTTGCACACTGAGATATAA  
 TAAAAGGTGTTTATCATAAAAA



**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRRLARRRKKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFRLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDVPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

10015010120130140150160170180190200

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCAC  
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAAGTTCAGTCAACATATTTTCATTGACTC  
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA  
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTTGAAGTCCCA  
 AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT  
 CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 AT**TAA**AATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA  
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
 TTAA

**FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVVSFWFGRRLLVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQIILED SMIFSLASCIITAKLCTWAICFLTTS EEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA  
AAGAAACCCTTCT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
ATTAAAAAAAAAAAAA

## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

10560-12201  
"let" 015101

**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC TTCACGGGTGC  
CCACTCAGGTCAC TTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TG**AGGCC  
CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

122/249

## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

protein" 01951001

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATC  
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGGCTCAGGCAGGGAGGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC  
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA  
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT  
 GCCCCGGGGCA



**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY  
YPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 125

GTGAATGTGAGGGTTTGTGATGACTTTTCTAGATGTCTAGGGAACAGAGAGTGGGTGCAGGGGGCCCCCA  
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGGAAGTGTGCGCGCCGCCGCCGCGTCTGCTCCTGCAGCGCTGTGACCTAGCCGCTAG  
CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
GGCTGCGGCTGCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCTCTACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCTTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGGTAAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
GAAAAGGAATTTACAGTTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
GTTAACTTGATGTAAATGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTTCTGGCTTTCTGGTG  
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGGAAGATCATTTTTTTCATCATTTGGATTGATGTCTTTTATTGGTTTTCTCATGGGTG  
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCATTTCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCCTTGGAATTAGTTTGTGTTGGTTCTTGTA  
AAAACCTTGGATTTTTTTTTCAGTAACTGGTATTATGTTTTTCTCTTAAATAAGGTAATGAA  
TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA  
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCCTCCGAGGGAAATCTTATACTTTATTGC  
TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTTT  
TCGCTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTTATTTATGTCTGTTATAGAATAAAGA  
TTAATATATGTTAAAAAAA

## **FIGURE 126**

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI  
SVRAANSKVAFAVRSTNHEPSEMSNKTRIITYFDQILVNVGNFFTTLESVVFVAPRKGIYSFSF  
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

protein database

**FIGURE 127**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CCTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACCTGTGCCTTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

### FIGURE 128

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF  
GIMSGVFSFVNTLSDSLGPGTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDGCCKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKLCLLCQDKN  
FLLYNQRSR

amino acids 1-19

amino acids 32-51, 119-138, 152-169, 216-235

## amino acids 120-123

amino acids 31-65

**FIGURE 129**

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTTCGCTCTGGGCTTGCCCTTCT  
 TGGTGTCTCTTGGTGGCCTCGGTTCGAGAGCCATCTGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG  
 AGTTTGTAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC  
 GCAACAGGACAGAGGGCGTGCCTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG  
 TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT  
 ACCAAAAAGTGAACGAACCTGTGTGAGCCCCCACCAAGAATGAGTCGGAGATTTCAGTTCTTCTACGTGGATG  
 TGTCCACCCCTGTCAACAGTCAACACCACATACCAGTCCGGGTGAGCCGCATGGACGATTTTGTGCTCAGGACTG  
 GGGAGCAGTTTCAGCTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT  
 CGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCCTGCTCAGTCATCTCCATTTCAGGATGTGCTGTGCTCCTG  
 TCTATGACCTGGACAACAACGTAGCCTTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC  
 AGCGCAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT  
 CCCTGCCTTTCTACCCCTTCGAGAAGATGAACCGGTGATCAAGGGGACCGCCAGAAAACCCCTGTGAGTGTGCTGG  
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCCTGGGTATATTTCTCTCCTTTTACC  
 TGCTGACCGTCTCCTGGCCTGCTGGGAGAACTGGAGGCAGAAGAAGACCCTGCTGGTGGCCATTGACCGAG  
 CCTGCCAGAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCCTTATGAGGTTTACAACT  
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG  
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG  
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTTCGCACCAAGCAATACCTCTATGTGGCTGACC  
 TGGCACGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT  
 TCTATGCCCTTCTGTGGTGCAGTGGTGTATCACCTACCAGACGGTGGTGAATGTCACAGGGAATCAGGACATCT  
 GCTACTACAACTTCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT  
 ACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA  
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA  
 TGGAGGGGCTGCTCAGTGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACACATCGTTTCATGT  
 ACATGATCGCCGGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG  
 CCTACGCCTGCCTGGCCATTGTCTCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTTCT  
 GGATCGTCTTCTCCATCATTACATCATCGCCACCCTGCTCCTCAGCAGCAGCTCTATTACATGGGCCGGTGGA  
 AACTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC  
 TCTACGTGGACCGCATGGTGTGCTGGTTCATGGGCAACGTCACTCAACTGGTCTGGCTGCCTATGGGCTTATCA  
 TGGCCCCCAATGATTTTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTTCGCTTCTACA  
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT  
 GGGGCTTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA  
 ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATTCTCG  
 GGTCTTCTCCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTTCT**TAGC**  
 AGGAGCTGGGCCCTTTCGCTTTCACCTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTCTGTGCT  
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT  
 GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCGAGGAGCAGGCCTGCTCCCCTGGAACCCCC  
 AGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTGGGGCCCTCCATGGGCCCCCTGTCTTTGGCTCTCCATT  
 GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCCTCCCCATTTTCATGCCTTGCATTTTGGCCGCTCCTCCCC  
 ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCCCTACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA  
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCC  
 AGGATGGATGGGGTATGAGATTTTGGGGTTGGCCAGCTGGTGGCAGACTTTTGGTGCTAAGGCCTGCAAGGGG  
 CCTGGGGCAGTGCCTATTCTCTTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT  
 TGAGAACCCTTCTGATTCAAGAGGCTGAATTCAGAGGTACCTCTTCATCCCATCAGCTCCCAGACTGATGCC  
 AGCACCAGGACTGGAGGGAGAAGCGCCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCC  
 AGCTGGTGGCCTTTTCAGTGCCATTGACACTGCCAAGAATGTCCAGGGGCAAAGGAGGGATGATACAGAGTTTCAG  
 CCCGTTCTGCTCCACAGCTGTGGGCACCCCACTGACCTAGCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTTT  
 CCTCTACGTGCCAGTCTTAGCCTCGCTTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAGGCA  
 AGTCTGTGTAGTCATGCACACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC  
 CCTGGCCACCCTGGTCTTGGATCCCCCTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGGAGCTCAGG  
 CGGGGCTCTGCTTTGGGGATGGGAATGTGTTTTTCTCCAACTTGTTTTTATAGCTCTGCTTGAAGGGCTGGG  
 AGATGAGGTGGGTCTGGATCTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT  
 TGCATTCAATAACAACCAGACTCAAAAAAAAAAAAAA

**FIGURE 130**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESH LGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFPYFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLELLIILQREINHNRRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPTYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTG  
 ACC**ATG**GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACC  
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA  
 GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
 CTTCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC  
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT  
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
 AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCT  
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGGCCAGGA  
 TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
 CCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTTCGAGTGATCGTGTGTGCTGCAAC  
 GTGGAGGGGAGTGATGCGCAAGGTGGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGC  
 AGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTCATTTCACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCCTGAAGGCG  
 ACTGTCT**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTCGCCCAATAATAAAGCCCCA  
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG



**FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPD MFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPF EVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRL SAEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLT AIDADLEPAFRLMDFAIERGDTE  
GTFGLDWEPD SGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGD TYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGAC**ATG**AGGTGGATACTGTTCAATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCGTGAGGCGGCCGCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTGCCTGTGGCCAAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA  
 GGTGAAATCAGTGGTAGATTTTATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
 GAGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGGGCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC  
 TTCCTCCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAGG**CGATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG  
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC  
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAAAGAACATC  
 TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT  
 TCGCAGTCTTCTGGAAAATATTTTCTTTTGAAGCAGCAAATCTTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTTGCC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA  
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAAGGCTGGTCTCAAACCTCCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCCCCGTCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCTTTCAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTTCAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCTAATGGGCTTACCTCCT  
 CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGTCTGTGGTGTATCCTGTGTT  
 TCCTTGTCTGGTTTG  
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT  
 GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTTGTTGTTTGTGTTT  
 TTGTTTTTTTTGCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

**FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

**Signal peptide:**

amino acids 1-16

1001564012201

**FIGURE 135**

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCAAA**ATG**  
 GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC  
 CCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCAC  
 AGGTGTATTCCCTCAACACCGACTTTGCCTTCGCGCTATACCGCAGGCTGGTTTTGGAGACC  
 CCGAGTCAGAACATCTTCTTCTCCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT  
 TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA  
 CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCCAGC  
 AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC  
 AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA  
 ACCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTT  
 GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT  
 TAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATATACAAGAAAGAACTTCCCATTCCTGG  
 TGGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG  
 GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT  
 CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTCAGCCAGAACAC  
 TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCC  
 ATTTCTGCCTCCTACAATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGA  
 CAAAATGCTGATTTTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC  
 ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG  
 TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT  
 GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAATATCCCA  
 CTAAATCC**TAG**GTGGGAAATGGCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAA  
 CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTGCTG  
 GCAGGGATGCCACTTCCAAGGCTCAATCACCAAAACCATCAACAGGGACCCAGTCACAAGCC  
 AACACCCATTAACCCAGTCAGTGCCCTTTTCCACAAATTCTCCCAGGTAAGTACTGCTTCATG  
 GGATGTTGCTGGGTACCATATTTCCATTCTTGGGGCTCCCAGGAATGGAAATACGCCAAC  
 CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAATATGAAT  
 TCAA  
 AAAAAA

**FIGURE 136**

MASYLYGVLFVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSK GKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

10015510:24204

**FIGURE 137**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGC  
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG  
 CCTTTATCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG  
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAG**ATGA**AGATGC  
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC  
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC  
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA  
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG  
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA  
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC  
 CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC  
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA  
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA  
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC  
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG  
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAAC  
 TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC  
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCA  
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG  
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCTCCAG  
 TGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCA  
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC  
 ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC  
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGAAGCCAGCACAGCCACCAACT  
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACT  
 TCCAGTGGGGCCAAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC  
 AGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGGCAA  
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCG  
 GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC  
 CTTTAACACAGCTGTCTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG  
 GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCTAACTGGTTCTGGAGGAGACCAAGTA  
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCT**TGAG**CAGCCCCGGAAGCAAG  
 TGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTTTATTTCATC  
 CCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCTCTACC  
 TTTCTTGCCTTTACCAGACACTGGAAAAGAGAAATACTATATTGCTCATTTAGCTAAGAAATAA  
 ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAG  
 CTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA  
 TCTCCACAGTAAATCCAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAA

## FIGURE 138

Signal peptide:

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAAT**ATG**CATCTTGACAGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCC**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTTGTGAATAAACTTGATACACCA



**FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
```

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHIGQAGKEAEKLGHGVNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

**FIGURE 141**

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC  
 CCCGCGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCCGGGGCGACTCG  
 GGGGCGGACCGCGGGGCGGAGCTGCCGCCGCTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC  
 GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG  
 CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTCCTGCTGTCAGCCGCCGCTCCGACCTGGGCGCTCAGC  
 CCCCAGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCCAACCTAC  
 ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTCTTGCAGCTCAGTAGC  
 AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGACAGCGCAGAGAAGAAACAGCAGTGC  
 AGCTTCAAGGGCAAGGACCCACAGCGGAGTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC  
 CTGTTACCTGTGGCACAGCAGCCTTTCAGCCCCATGTGTACCTACATCAACATGGAGAAGTTCACCCCTGGCAAGG  
 GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC  
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGGAATGACCCGGCCATCTCGCGGAGC  
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC  
 ATTCTGAGAGCCTGGGCAAGCTTGAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA  
 TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
 CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCCCGACGATGGCTTCCCTTCAAC  
 GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT  
 TCCCAGTGGCACAGGGGAAGTACAGAAGGCTCTGCCGCTGTGTCTTCACAATGAAGGATGTGCAGAGAGTCTTC  
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG  
 CCTGGAGCGTGACATCACCAACAGTGCCCGGAAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCCGCGTGCTG  
 AACTTCTCAAGGACCACTTCTGATGGACGGGAGGTCGCAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC  
 TACCAGCGCTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC  
 GGCCGGCTCCACAAGGCAAGTGAAGCGTGGGCCCGGGTGACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA  
 CAGCCCGTGACAGATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG  
 GTGCCCATGGCCAAGTGCAGCCTGTACCGGAGCTGTGGGAGTGCCTCCTCGCCCCGGGACCCCTACTGTGCTTGG  
 AGCGGCTCCAGCTGCAAGCACGTGAGCCTCTACAGCCTCAGCTGGCCACAGGCGGTGATCCAGGACATCGAG  
 GGAGCCAGCGCCAAGGACCTTTGCAGCGCTCTCGGTTGTGTCCCGCTCTTTGTACCAACAGGGGAGAGCCA  
 TGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTGCCGCTCCTCTCCAACCTGGCGACCCGA  
 CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCAGTGTACCCACTGGGGACCTGCTGCTG  
 GTGGGCACCCAACAGCTGGGGGAGTTCCAGTGTGGTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC  
 TGCCCAGAGGTGGTGGAGGACGGGGTGCCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA  
 TCGCGTGTGAGTGCACAGCTGGTGGCAAGGCCAGCTGGGGTGACAGAGTCCCTACTGGAAGGAGTTCTGGTG  
 ATGTGCACGCTCTTTGTGCTGGCCGCTGCTGCTCCAGTTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA  
 GTCTTCTGAAGCAGGGGGAATGTGCCAGCTGCACCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC  
 CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG  
 GGGGCCCCAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG  
 TGCCCCCGGCCCCGGTCCGCTTGGCTCGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC  
 TGCCCTGGCTTACAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGTGAAC  
 ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC  
 TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCCTAGGTTGGTGGAA  
 CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAACAATTCCAATGTGAACTAGAATGAGAGGGAAGAG  
 ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTATGGCCTCCCAGGGGTGCTGGGGATGCATCCAAGTGG  
 TTGTCTGAGACAGAGTTGGAAACCTCACCACTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC  
 CCTGTCTCACTGCAGATTCAGGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCAGTCAGCCGAGGATGTAGTTG  
 TTGCTGCCGCTCGTCCCACACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCCTGGGCTC  
 GGACCCAACCTCCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA  
 TTTCTGTACAATGTACGCCTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA  
 GAACCCGTGTGCCCTTCCCACCATATCCACCTCGCTCCATCTTTGAACTCAAACACGAGGAAGTAACTGCACC  
 CTGGTCTCTCCCAAGTCCCACTTCCACCTCCATCCCTCACCTTCTCCACTCTAAGGGATATCAACACTGCCC  
 AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCTATTTTTTAATAAA  
 GTCTGAAGAATTACTGTTTAAAAAAAAAAAAA

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962  
><subunit 1 of 1, 837 aa, 1 stop  
><MW: 92750, pI: 7.04, NX(S/T): 6  
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCF  
FDPNFKSTALVVDGELYTGTVSSSQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSQYQP  
QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPCEQVQFQPNNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA  
 GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCGCCCGTCTGCGCGCTCG  
 TGCCCGCCCCCGCTCCCCGCGCGCGAGCGGGAGGAGCCGCCACCTCGCGCCCGAGCCGCCGCTAGCGCGCGC  
 CGGGCATGGTCCCCCTCTTAAAGGCGCAGGCCGCGCGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGGG  
 CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGGGCGGGCCGCGGCGGGCGGGCGCTGCCCGGGCGGGCCCTCG  
 CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGCTGAGGGCGCGCGGAGCCTGCGGCGGGCGGGCG  
 GGCGCGCGGGCGGGCCCGCGGGCGGAGCGGCGCGGGC**ATG**GGCCGCGCGCGGCCGGCGCGCCTGGCTCAGCGTGC  
 TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG  
 GCCCACGGGCGCGGCCAGCCCCGAGGGCTGCCGTCGGGACAGCGGGCGGCTTCCAGGCCGGCGGGGCGCGCG  
 GCGATGCGCGCGGGGCGCAGCTCTGGCCGCCCGGCTCGGCTGATCATGAGCCGGGAGGTGCTTCGGAGAATTTCTCT  
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA  
 TTCCTGGGAAAGTTTCAAGTCTTCTCAAGTGAAGGTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG  
 GTGTGGACGACTCCTACCCGCCCCAGAAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAATTCCTGAGGAGTT  
 TGAACAGCAGCGAGCCCCCTTTTCTTGGGCAGACAGGCTGGGCACCACGGAAGAAATGGGAAACTGGCCCTGG  
 AGCCTGGTGAGAACTTCTGCTAGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATTCCTCCCGC  
 ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG  
 CAGGGGTGCAAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAAACAAAAGGGGT  
 ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACACCCCAACAAAACCCACCTACCAGT  
 ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA  
 TTGTCCTGATGAGCAAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA  
 TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACCTGTATTCGGCAG  
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGACGACATTGTCTATGCAGGTCA  
 TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATATTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
 GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAGCACAAAGGGAAGAAAA  
 TGACGCTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
 TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTCTCTCAAACCTCCCTGAAGA  
 AGCTCGTCCCCTTTAGCTCCCTGGGTGCAAGAGTGAGCACAAAGAACCACAAAGATAAAAAGATAAAACATACTGA  
 TTCCTTTGTCTGGGCGTTTTCAGCATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCAATC  
 AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCCCTGACAAGGCCAAACAAAGTTGAAGTATGA  
 GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTTCAGAGCCCTGG  
 CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTCTGCGACGCTGACCTCGTGTTTACTA  
 CAGAATTCCTTCAGCGATGTGAGCAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTCTGTTTACAGT  
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAACCTGGCTTCT  
 GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA  
 TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC  
 AGGAAGTAGGAGTAGTCCACGTCCACCATCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT  
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA  
 GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCC**TAA**TGTCCAGCTTTGCTGGAAAAGACGTTTT  
 TAATTATCTAATTTATTTTCAAAAATTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC  
 AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTCCTTTGAA  
 CACATCTTCTTGTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAAATGTACCTGATGAACAAAACCTTT  
 TTTAAAAAATGTTTTCTTTTGGAGCCCTTTGCTCCAGTCTATGGCAGAAAACGTGAACATTCCTGCAAAGTAT  
 TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTTGT  
 GTTTTGTTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
 GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC  
 CACGTAGGTTTTTTGTTTTGTTTTGTTTTGTTCTTTTTTGGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG  
 CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATTCCTTGCCTTTGCCTCCCGAGT  
 AGCTGGGATTACAGGCACACACCACCGCAGNTAGTTTTTTGTATTTTGTAGTAGAGACGGGGTTTACCAT  
 GCAAGCCCAGCTGGCCACGTAGTTTTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG  
 TGGTAGTTTCAATCGGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTTCTCTTGCACCTT  
 CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT  
 GAAACATACACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTCATCCTGTCTG  
 TGTATGTGGGTGGAGATGTTTTTCACTCTTTCATTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA  
 TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG  
 GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTTTCCCTCC

**FIGURE 143B**

TTAATTTTATATTCCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG  
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTGGGAAAAATAAACAGTGAACAATATTTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT  
ATTCCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAA

1001560 "143B" 1001560

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALPEGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT  
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE  
ILEWEFLTGTKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFSLNSLKKLVFPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
 TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
 ACGGACGACGCCT**ATG**AAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC  
 TAACTCTCCAAAACATGTTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA  
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAAACACACGGAAAGTACCCC  
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC  
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
 CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTTTGAAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC  
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA  
 TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
 AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
 ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAA

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKHTSTPFWSI  
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTSSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

100560-2120



**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA  
 GGAATATCC**ATG**GCCTTTTGTGCTCATTGTTGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCCAGATTTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA  
 GGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACAATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC  
 ATTCATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
 CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTGGGGAT**TGA**GACAGAGAAGACCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC  
 CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTGTGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTTGCCTCACAGGTGAAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTTGCAGGTTTGAAGGACAGTGTTTGCTAATGATGTGTTTTTA  
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTTATTCCACATTAATTTACTTTTCTCTA  
 TACCAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
 GAGGTAGGATTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAACCAGGCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
 TTCTAAATAAAATTTTAACAAATTAACTAAACAATATATTTAAAGATGATATATACTACT  
 CAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAATT  
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA



**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA  
 TTAATAAGCACATTGTCATTTACAACAGCAAACTATATGCTGAGTTTGGCAGAGAGGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAG  
 AATAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA  
 GATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
 GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG  
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**  
**AG**AGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGCTTGATGCATGTATTTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
 ACTTCATCATTTAGGAAGTATGGGAACAAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA



**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCTCAAGACTTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCGCGCGCCTGCCTGTGCCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCCGACCCGCCGCGCATGGGAGAAGTGCGCATTTGCGG  
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCTCCACTACTGG  
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTATGTCTGTTGCGTAGTGGCCGCTA  
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
 CCTGCCTTCGGGCCTTGACGCCGCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC  
 GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGCGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**  
 AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
 GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA  
 AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874  
><subunit 1 of 1, 238 aa, 1 stop  
><MW: 25262, pI: 6.44, NX(S/T): 1  
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPGLSSPAQPPDPMPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA  
AQKGPPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVPOAGGEGLEGADIPAFGPC SRL  
AVPPNPRTL VHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGG  
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGTCATGGTACT  
 TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACTTATGGTTCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAAACAACCTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC  
 CTTGAAGAATGACAACTCTCAGCACCTGTCACTGTCCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTA**TAAAA**AGAAATGTACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGAAAAGTTTCATGTCATAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT  
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA  
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAATTAGTCGATTTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
 GAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG  
 AAGACTCTTTTTGACACTAAACACTTTTTTAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA  
 GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTTCCTTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA  
 ATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAAGAGTATAGTATATTTATTT  
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTCTCAGAATATGGAA  
 AGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA

**FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ  
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF  
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGETDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
 TGCACCTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG  
 TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC  
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT  
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGGTCAGCATCCAGTACGA  
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCAGGCAGCCCCT  
 GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC  
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA  
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
 GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTGCAGTGCTGGGAGCCGCTTCCTTCCTG  
 CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC  
 CTCTGCCCACAGCCTCAGCATTTCTTGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC  
 TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
 CTGGCAAAAAAAAAAAAA



**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG  
 AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC  
 TTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCA  
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  
 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG  
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA  
 AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTACA  
 CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCATCTCGG  
 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG  
 GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC  
 CTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCC  
 AGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  
 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGC  
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGTCTGTCTCCCGCCGATTCTCCCA  
 CAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT  
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA  
 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCT  
 TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATA  
 CACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCAACACAG  
 GGTGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC  
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTGTAGGCTTCTCAGGAGGTGTCTGGA  
 GGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCGGGACCCCCACTGTGCCT  
 GGGACCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCCGAAATCATT  
 AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT  
 GGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG  
 ATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG  
 ACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  
 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCT  
 TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG  
 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG  
 AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA  
 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG  
 CAGCACAAAAGACCACCTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
 ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC  
 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTC  
 CAGAAACACAGTGTTCAGAGACCCTAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAACATC  
 TAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTGGACACCAACACTCCCT  
 TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC  
 TTTCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAAATGG  
 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT  
 TTTGGGATTGAGAAACTGCTGTGAGAGACTGTTATTTTTTATTAAAAATATAAGGCTTAAAAAA

**FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ  
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA  
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE  
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGSLHKAVVSGDSSAHLVEEIQLEFPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRAN  
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP  
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
HFVTVTVLFLVLGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
SASDVDADNNCLGTEVA

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA  
 GTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
 CATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT  
 CAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC  
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA  
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTGAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAATGTGAAAATTGTGGA  
 CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG  
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCACCATTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC  
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
 TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT  
 CTTGTCCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA  
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATATTCTTTCAGTTTCTGTTT  
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGC  
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA  
 GCGTTATCTCTCCCCAACCTCACTAA

**FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV  
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF  
INSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPQGVWKCQCShwPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ  
NSIMEAIIQHGVPVVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFPQWPWHEQYLFDFVFLGLT  
LGTLWLTCGKLLGMAVWWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT  
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTGAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA  
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC  
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
 GGGTGGGCCCAGGAGGGGTCAGAGCCCGTCCCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
 GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
 ACCAGTGGGGCCATCTACTTCGACCAGGTCCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
 CTCTGGCTCCTTCGTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG  
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA  
 CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT  
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCT**TGA**GGACCCAAGTCTTTCAAGCACAGAAT  
 CCAGCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA  
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACC  
 CTCCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
 AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCACCCAGCTTCCT  
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCCAG  
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTGAGGAAAGCCAGCATCACGGATC  
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTTGTCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC  
 CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCCTCCCAGCTCTC  
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTTCTCCTGAT  
 CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTATTACCTGGGATTCCATGATTCAATCCTT  
 CAGACCTCTCCTGCCAGTATGCTAAACCCTCCCTCTCTCTTTCTTATCCCGCTGTCCATT  
 GGCCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA  
 TGTTGCAGAGGAAAATAAATATCAAAGTGTATACTAAATTAATAA

**FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECCLVVCEPGRAAAGGPGBA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32

10056404200



**FIGURE 163**

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCCAGC  
 CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGGCAT  
 GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGGCCGTGACTGGGCGGGCTTCAGCC**AT**  
**G**AAGACCCTCATAGCCGCCTACTCCGGGGTCCTGCGCGGCGAGCGTCAGGCCGAGGCTGACC  
 GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGTGCGCGAGGGGTCTGGGAGATGGGGCACT  
 GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTTCTCTGTACCTGGCTCAATAGGTCCAA  
 GGTGGAAAAGCAGCTACAGGTCATCTCAGTGCTCCAGTGGGTCTGTCTTCTTGTACTGG  
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG  
 CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTCACA  
 GTGGGTCCGAAACTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCCCATCCAGCTGGTGA  
 AGACACACAACCTGCTGACCACCAGGAACCTATATCTTTGGATACCACCCCATGGTATCATG  
 GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCCAGG  
 CATACGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTTGAGGGAGTACC  
 TGATGTCTGGAGGTATCTGCCCTGTGAGCCGGGACACCATAGACTATTTGCTTTCAAAGAAT  
 GGGAGTGGCAATGCTATCATCATCGTGGTTCGGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC  
 TGGCAAGAATGCAGTACCCTGCGGAACCGCAAGGGCTTTGTGAAACTGGCCCTGCGTCATG  
 GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC  
 GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCCAGAAATACATTGGTTTTGCCCC  
 ATGCATCTTCCATGGTCGAGGCCTCTTCTCCTCCGACACCTGGGGGCTGGTGCCCTACTCCA  
 AGCCCATCACCCTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG  
 CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA  
 CAAGACCAAGTTCGGCCTCCCGGAGACTGAGGTCCTGGAGGTGAAC**TG**AGCCAGCCTTCGGG  
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTTTGCTCTGTAAATTTGGAAGTGTCA  
 TGGGTGTCTGTGGGTTATTTAAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA  
 AA  
 AAAAAAAAAAAAAAAAAAAAAA

**FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM  
PGKNAVTLNRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK  
HKTKFGLPETEVLEVN

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-  
245, 318-323, 378-383



**FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFEVVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV  
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK  
YEADMVRRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN  
FLSWATILLSPLFSFVLGVFASGSPLLLITFLGFVGAASFGVRRLIGESLEPGRWRLQ

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

**FIGURE 167**

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTCTTCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTTAATGCTCTCATAAGACCACTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCAGTAGGCCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

**FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234  
><subunit 1 of 1, 143 aa, 1 stop  
><MW: 15624, pI: 9.58, NX(S/T): 0  
MHHSLQCPGAATRHILCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRR  
EGKINFYTNWGLRGPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGLSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

1005610-1204

**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAAGCCAC  
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
 ATTAAAATCTGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGT  
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
 ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
 ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGTTA  
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTT  
 CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT  
 CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
 TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
 GGGAAAGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAGGC  
 ATCGAGTCTCCTGCATTGAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG  
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC  
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
 GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG  
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
 AAAAATAAAAAAAGAATTATGGTTATTTGTAA

## FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
```

```
><subunit 1 of 1, 109 aa, 1 stop
```

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLPTLKS VFC SLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15



**FIGURE 171**

GCGGGCCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT  
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
GCCCCCGAGCTGGGACGGCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC  
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
**CTAG**GGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC  
CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282  
><subunit 1 of 1, 262 aa, 1 stop  
><MW: 28809, pI: 8.80, NX(S/T): 1  
MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS  
MREHPALRSLRLLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL  
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA  
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS  
LLPLGDGLTLAFKI

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

**FIGURE 173**

CCGCCGCCGCGACGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCCTGGGCCTCTCGCCGTCA  
G**CATG**CCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCTCAC  
TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCC  
CATCTTTTTCTTTGGCACACACGAAACAGCCTTCTTGGGACCCAAGGACCTGTTCCCTACG  
ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG  
GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCTCCGACAG  
CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG  
GGGTCTATGGCCGTACACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC  
GGTCTCGAAACGAGCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCG  
AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAAGACCAGCGACCAGGACTTCACACCT  
GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGGACGGAAAAAAGAA  
GGCGCCGTCAGCCTCCGACTCCGACTCCAAGGCCGATTCGGACGGGGCCAAGCCTGAGCCGG  
TGGCCATGGCGCGGTTCGGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG  
TCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG  
GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
TGGACCGCATCAGTGAGTGGAAGCGGCGGACGAGGCGCGGAGGCCGCGAGCTGGAGGCCCGG  
CGGCGGCGAGAGCAGGAGGAGGAGCTCGGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA  
GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGGCGGCAGCAGCGGGG  
ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT  
CCCCCGTCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC  
GAAGAAGCCGCAGTCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG  
TGCGGCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC  
GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT  
GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTGCAGACGCCGGACGTGAAGAGGT  
GCCTGAATGCCCTAGAGGAGCTGGGAACCCTGCAGGTGACCTCTCAGATCCTCAGAAGAAC  
ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA  
GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCGG  
TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG  
GAGCTGGCCGGGGGAGGAGGCCCCCCCAGGAGAAGGCCGAGGACAAGCCCAGCACCGATCTCTC  
AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGGAGAGCGCAGAGGACAAGGAGCACG  
AGGAGGGTTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC  
GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCAGAGGGGCACG  
GGGGGACTCGGAGGCCCTGGACGAGGAGAGCT**TGA**CCGCGGGGACGCCAGGCCAGCCCCGCG  
CCGAGCTCAGGCTGCCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGG  
GAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTTTTTTTTTCTCCTGCCTAATTTCTGTGATT  
TCCAACCAACATGAAATGACTATAAACGGTTTTTTTAATGA

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPKNKYPIFFFFGTHETAFLGPKDLFPYD  
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRG  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSSSDSDSVSKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAKPVKVERTKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE  
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

**FIGURE 175**

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
 ACACCATTTGAAAGAGAACATTGTTTTCATC**ATGA**ATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
 TTTTCACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA  
 AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTTCATC  
 AGAAGGACTGGATTTTCAAACCTCTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT  
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA  
 ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA  
 AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
 GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC  
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT  
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT  
 AGGAGGACAACGCAGCCTGATAAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG  
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTTATTACTCCCCACAAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT  
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT  
 TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA  
 TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT  
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA  
 TGTAAATGTTTCTTGAACAGACATTGGAACGTCTCAAAGTTGTGCTGTTTGTGTGTATAGCATGGCTGACAT  
 AGAGGTAGTCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA  
 GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCAGCTCTCCTTGCACAGATGCCACACTTATGGGAAAGC  
 TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC  
 TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTGTCTGGGACATCGAAGACAG  
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
 TAAATCCCAACAAGCAACTATTAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGAGTTGAAGCCCGA  
 TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG  
 CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA  
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA  
 CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCCAACAGATGTGGCAGAGGGAGAAGCG  
 GAGACAGAGAAACAAGGGGGGCCCAAGTGGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACG**TAG**TTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC  
 TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG  
 CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACCAGTTTT  
 CCAAGAACAATCTTGACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA  
 TGTTTTGAGTTTTTGAATTTTATGTAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
 GCTTTATTCCCTCGAATGTCCATTAAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT  
 CATTCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACCTCCCATATC  
 AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC  
 TGGCCACTGGGGTTAAATTTAGTGTAATAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
 ATTGACTAGTCAGGAGTAACAGGTTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA  
 GCTCTACAGGGACAGAATGCTTAATAAATACCTTAATAAGATATGGGAAATATTTTAATAAAAACAAGGAAACA  
 TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT  
 AAATTCTGGCTTTGGGGAAAACCTCATATCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA  
 TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA  
 AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC  
 AATGATATTTTCAGTATATATTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC  
 CTTTATTTCTCTCTGTATATTGGATTTTGTGATTATATTGAGTGAATAGGAGAAAACAATATATAACACACAGA  
 GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAATAATTTAAC  
 AACGGAAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT  
 GTAGTATTGTTTTTGAATTTAACAATAAATAAGCCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL  
GSSEGLDFQTL LLD EERGRLL LGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD  
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHHYIRTDISEHYWLNGAKFIGTFF  
IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQORSLINKWTTFLKARLIC  
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP  
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV  
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE  
LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA  
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA  
TIKWYIQRSGDEHREELKPDERRI IKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLT LN  
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
KGGPKWKHMQEMKKKRNRHHRDLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTATCCTGGAGCATGCCACCGCGGGGAGCAGA  
 CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC  
 CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCAAGA  
 GTGGCTGGAGAAAAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTACTACAAGATCCAGAACCATGGGCATC  
 GGGTGAGGTGGGGGGGCACAGGTGTATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA  
 GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGCTTCCTAGTTCTGTAGCCCCAGGT  
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
 AGGGAAGATTAAATGACATAATGTATGTG**ATG**CAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG  
 TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT  
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC  
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
 TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC  
 CCAAGCCCTGGCCACGAGGGCCCTCCCCTGCCCTGCACACGTGGTATTTGCTATCAGGCAGGGCGTGAGGATG  
 AGCTGACAATCACGGAGGGTGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
 ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC  
 AAGACAGTGACAATCCCTGCGGGGCAGAGCCCACAGCATTCTTGGCACAGGCCCTGTACAGCTACACCGGACAGA  
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGGCCAAGATGGAGTAGATGACG  
 GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTTGGGGTCTTCCCCTCCCTGCTGGTGGAAGAGCTGTGGGGCTGGCCCC  
 CAGGGCCACCTGAACTCTCTGACCCTGAACAGATGCTGCCGTCCCCTTCTCCTCCCAGCTTCTCCCCACCTGCAC  
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG  
 ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGGATCCTGGCCACC  
 CAGATCCCCTCACCT**TC**AGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCTTATCTTCAAGCTGTGAGA  
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCTCACCTCCAAGGGT  
 GGAAACTTGGCCCTTCCCATTCTAGAGCTGGAACCCACTCTTTTTTCCATTGTTCTATCATCTCTAGGACC  
 GGAATACTACTACCTTCTCTTCTGTATGACCCTATCTAGGGTGGTGAAATGCCTGAAATCTCTGGGGCTGGAAACC  
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCCTGGCTCCATGACCCACCCCACTCTGGATG  
 CCAGGGTCACTGGGGTGGGGCTGGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
 CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGGGCTCTTGTG  
 CTAAGAGGGCAGGGGGCTACGGTGTCTATTGCTTTAGGGGGCCACCAGGGCAGGGGGCTGCTCCAGCTGCCAC  
 GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC  
 TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC  
 AGCTGGGGGCGAGTGTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
 TCCATCAGCACAAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCCTGTTCAAGCTGTGTCCAGC  
 TTTTCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC  
 AGTTTACTCTGGGGTTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG  
 TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCCAGCCAGTGC  
 AGTCCCGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGGCTGGCTGCCATTGCTCTTGAGTGG  
 GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCTTCAAGTG  
 CACGAGGGGTTAGGCTGCTGTCCCTGAGTCCCTCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC  
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG  
 GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT  
 TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG  
 GCCCTCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC  
 AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCCACTT  
 TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA  
 CAGAGAACACAGTGGTCTCCCCTGTCCGGGGCGGCTTTTTCTTCCCTGGAGCGTCCCTGACGGACAAGTGGAG  
 GCCTCTTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC  
 CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT  
 TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCCAAGCCCCAATTTCCCAAGCCCCATTT  
 TTTCTGTCTTTATCTAATAAACTCAATATTAAG

FSPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

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2098年	100
2099年	100
2100年	100



**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA  
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG  
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTCTCTTAACGGTCTCAGCCCTTCTGAAAACCTTTGCC  
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCC**ATG**TCCAGACAGGCTCGCATCCCGGGAGGGG  
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG  
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCGGCTGGCCAGCCCCCTCCCGGGAGGAGAGAT  
CGTGTTCAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA  
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGAGGGGCTGACAGTGCAGTA  
CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAACCTCA  
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC  
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCAAGAGCCAA  
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC  
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCACCCAAGCATCCGCAATCC  
TGTCAGCTTGGTGGTGAATCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGGCCCCAAGTGGGGCCAGTGTGC  
CCAGACCTGCGCAGCTTCTGTGCCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTTGA  
CACAGCCATTCTGTTTACCCGTGAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGGG  
CACCCTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA  
TGAAGTGGGTGATGCTTCAACATGCTCCATGACAACCTCCAAGCCATGCATCAGTTTGAATGGGGCTTTGAGCAC  
CTCTCGCCATGTGATGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT  
CATCACTGACTTCTTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT  
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTGGGGCCGACTCACGCCATTGTCC  
ACAGCTGCCCGCCGCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA  
CTCGCCCTGGGCCGATGGCACACCCCTGCGGGCCCCGCACAGGCTGCATGGGTGGTGGCTGCCCTCCACATGGACCA  
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTGAATGCTCTCGGACCTG  
TGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG  
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
GTGTGCTGCCATAACACCCGACCGACCTCTTCAAGAGCTTCCAGGGGCCATGGACTGGGTTCCTCGCTACAC  
AGGCGTGGCCCCCAGGACCACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC  
ACGGGTGGTAGATGGGACCCCTGTTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATGCCATGGCTG  
CTGTGATGCGATCATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCTG  
CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCCGGGGGGCCACCCA  
CATTCTTGTCCGGCAGCAGGGAAACCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA  
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGGCCTA  
CAGCGGGGCACTGCAGCTCAGAGACACTGTGAGCCACTGGCCACTGGCCAGCCTTTGACACTGCAAGTCTCT  
AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTCGTGCCCCGGCCGACCCCTTCAACGCCACG  
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG  
GAAAT**TAA**CCTCACTATCCCGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT  
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT  
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCACTGATGGGTAGTGGATGGAAGGGGCTGACAGAC  
AGCCCTCCATCTAAACTGCCCCCTCTGCCCTCGGGTACAGGAGGGAGGGGGAAGGCAGGGAGGGCCTGGGCCC  
CAGTTGTATTTATTTAGTATTTATTTACTTTTATTTAGCACCAAGGGAAGGGGACAAGGACTAGGGTCTTGGGAA  
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG  
TGTGTATGCGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTCT  
TTCCTGAATTTTATTTTGGGAAAGAAAAGTCAAGGGTAGGGTGGGCTTACAGGAGTGAGGGATTATCTTTT  
TTTTTTTTTCTTTCTTTCTTTCTTTTGTGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG  
GCACAATCTCGGCTCACTGCATCCTCGCCTCCCGGTTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG  
GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTTGTGTTTTGTTTTGGAGACAGAGTCTCGCTATTGTC  
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTTCAGCAATTCTCCTGCCTCAGCCTCC  
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGGCTAATTTTTGTATTTTGTAGTAGAGACGGGGTTTAC  
CATGTTGGCCAGGCTGGTCTCGAATCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAAGTGCTGGGATT  
ACAGGCGTGAGCCACCGTGCTGGCCACGCCCACTAATTTTTGTATTTTGTAGTAGAGACAGGGTTTTACCATTGT  
TGCCAGGCTGCTCTTGAACCTCCTGACCTCAGGTAATCGACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
TGTGAGCCACCACGCCCGGTACATATTTTAAATTGAATCTACTATTTATGTGATCCTTTTGGAGTCAGACAG

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAGGAAA

[illegible]

**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV  
 FPEKLNQSVLPVPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP  
 GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP  
 ASGQGPNCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA  
 AAKAFKHPSIRNPVSLVTVRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF  
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD  
 NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG  
 PAQACMGGRCCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTCAGGVQFSSRDCTRVPVRNGGKY  
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRDLEFKSFPGPMDWVPRYTGVAPQDQCK  
 LTCQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG  
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNPGHRSIYLALKLPDGSYALNGEYTL  
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
 PSTPRPTPDWLHRRQAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
 582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA  
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 37130, pI: 5.18, NX(S/T): 3  
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY  
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT  
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI  
NPTLISVSELQDFEEEGEDLHF PANEEKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY  
TENGIEFDPM LDERGYCCIIYCRNGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV  
ARMLGRV

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
GCGCCTGCGCCGTATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA  
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
GGCACCTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGAG**TCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

10015610151201

**FIGURE 185**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
 GTCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCGTG  
 GGCTGGGTGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG  
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
 ATATACGATGGAGGTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA  
 AACAAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
 TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
 TGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG  
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG  
 TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
 TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT  
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA  
 ACTAATTCTTTAA



**FIGURE 186**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
```

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG  
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATGG**CAACCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG  
AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC  
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGGT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTTTTAACTTTACTATAAAGC  
CATGCAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA  
CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTCAAGGATGAGATATTAAACCCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAGCATCTACTCTTTTTTATCATTTACTTCAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAAGTCAACTATTGCTTTTTCAGGGAAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATATAATGA  
AGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTT  
TTCTTGTGTATTAAATTAACATTTTTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGTTTAGTTTTACTAAA  
ATCTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAACTGACAATCCAATTTGA  
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA  
TTAATAAATTGTACATTTTTTCTAATT

**FIGURE 188**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
```

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTTGACACTGCTGGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCTACCTCTGGGA  
TTGTCTTTGTTCATCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT  
GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTC**TGA**CGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTGAAGGATATTTAAATTCATTT  
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC  
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCAGTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAAGTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACACTCACATTTTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

**FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
```

```
><subunit 1 of 1, 220 aa, 1 stop
```

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM  
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLPVCWTAHAIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP  
SGGSQGPHSHMARYSTSAPAIRGPPSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAAGGAGAACATCATCAAGACTTCTCTAGACTCAAAGGCTTCCAGTTCTACATCTTG  
AGCATCTTCTACCACTCCGAATTGAACCAAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC  
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCT  
TGCGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACTTCAGGAGTCTCTTTCATCCTGAC  
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT  
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA  
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

**FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

10015640-12201

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA



**FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
```

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN  
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

[illegible]

### FIGURE 195

CCCGCGCCCGGGTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTC  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGTTTCTGATTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

### FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
```

```
><subunit 1 of 1, 148 aa, 1 stop
```

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKLMLQKREAPVPTKTKVAVDENKAKEFL

GS LKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEY YGDYYQRHYD

EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

[illegible]

## FIGURE 197

CGGCTCGAGCCCCGCGGAAGTGCCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTG  
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCCCTGCCTTCTGGTGCTGGCCCTTGCCCTGGGTCTCAACGCACA  
CCGCTGAGGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTACAGCAACACCGCCAG  
CCCCGGACTCCCCGCAGGAGCCCCCTCGTGCTACGGCTGAAATTCTCAATGATTGAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG  
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCTGCCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCCATGTACCGCCCGTTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC  
GGACCTTGCTCCCCGCGCCGCGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCCGGGGCTCGGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCCGA  
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA  
AAAAAAA

## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRRLKFLNDSEQVARAWPHDT  
IGSLKRTQFFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

### **Signal peptide:**

amino acids 1-31

### **Transmembrane domain:**

amino acids 195-217

10015610-12201

[illegible]

**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

10015610-121201

**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
 CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
 TTGGGGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGCACACGC  
 TGTGGCAAATGTCAGGACCAGGTAAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
 CTGTTGCATTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT  
 TGCACCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGAGCCTGGACCCAC  
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCCGAGGTGCGG  
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
 CCAGGGCCTTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCCCTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
 GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTTCCAT  
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTGCGATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG  
 TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAC  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT  
 GTCCCATGGTGTGGCTCCTTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC  
 AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA  
 GATAAATGCTGTGGATGAACGAT**GTA**ATGTCAATGTGCAAGGAAAAGAGAATTTTGGCCATC  
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT  
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA



**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP  
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDQSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLGCRTFHWFLANVYPEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEEGLAIHQQHWFQENGMIVHILSGKCMEEAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCTCCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG  
 CACCCACAGCCACCCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTGCAGCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGGACCTGCCACCCTGCGGCCATT  
 CTGTTGCGGGGCCGTGGGGAAGGTGTGGACCCCAAGTCTATGTGACAATTACCATCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCAACCC  
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CTTTCCAGTTGAACCGG**TGA**GGGCAGGGGCAATGGGATGGGAGGGGCAAAGAGGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
 CTCCCACAGCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATTCTCTGCTGCCCATAACTCCAACCTCTGCCC  
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCCTTCTATTCTGGCCTACCCCTTGTTTCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCCCTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCCTCACATATCTGTGACTTCG  
 GGTCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC  
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCACATTTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGACACTTTACCTCTCATGTGCGTTTCCCGGCCCTGATGTTGTGGTGG  
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGGCCCTCATCGGTCTATGG  
 TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCAAGCCCA  
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG  
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTTCCAGCCT  
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGGACTCCCTCCTGTCCCCCTCCTTT  
 CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTTGGCTTCCCTTCCCTTCCCTTCCCTCAGGTT  
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTTCCCTTCCCTTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATTATCTCTTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

**FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

1005640:2204

**FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGG**  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACC GCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA  
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

T02T2T025T02T

**FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG  
PPAPT VAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC  
CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG  
ACTCGCACGTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC  
CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTTCAGGGGCGCACCACTTCCAAGCCTGTGT  
CCCACAGGTCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC  
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCTTAGAGGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER

HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

20150424

**FIGURE 209**

AGCAGGAGCAGGAGAGGGACA**ATG**GAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTATTCAACAGCG  
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAAACTTTTGTGATGGATTCTTAAGTGGAATAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**CTGA**CTTCTCCTTGGAACACATATGGCC  
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG  
 GATCACTAGGCCTGCCAACCACACACACACACGACGTGCACACACGCACGCACGCGTGCACAC  
 ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAAATCTCGTTTTCTC  
 TTCTTCCTTCTTTTAAATTTATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
 ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCC  
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA



**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHVMTEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

1001560-2401

## FIGURE 211

GGAGAGAGACCGCGGCTGGGACCAGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACATGGCAGCGTCCGCCGGAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG  
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTTTTTTCCACTACTC  
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
TATATCTGTGATGTCAAAAACCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCACCAGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC  
CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA  
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC  
AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTCCACATCATTTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAAATCTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACT  
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
AAATGTGTCATATCAATTTCTGGATTACATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG  
GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT  
GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

**FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKDDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

10015610-121201

**FIGURE 213**

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCCGGGCTGCCGCC  
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGCGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA  
 TATGAAGGTGAAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGAATTTCG  
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT  
 ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA  
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT  
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
 ACTTTTGGCTATACCCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
 CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
 TTAACACTATTTTATTAATTAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
 TGTTTATAAAGTAAAAAAA

**FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

## FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCGATGCACGCGTACGTAAGCTCGGAATTTCGGCTCG  
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT  
GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
TGGAGTCGCACCTGTTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACACAGCCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCTCATGATGTCAGG  
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG  
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATTCAGTGTCACTTGATACGTTATTTCAGAAACCCAAG  
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEA  
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELENTSVQ  
LQPPTTAPGPETAFAFIERLEMEQAQKAKNPQEOKSFFAKYWYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGGSGLCCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

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**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGCAGCAGGTCGTCCGGGGGCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA  
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA  
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTCGGACCGCCGC  
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
CTGGACACCTGTGCTGGACCCACACGGGGCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAGCATTTGCTCTG  
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT  
GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA  
ATAAACACTTTTAAATGATCAAAAAAAAAA



**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLEMLTFSTSPGQESPVESFIAFLLIELACGLYFSPMSFLRRKVIPET  
EQAGVLNWFRVPLHSLACLGLLVLHDSRKTGTRNMFISCSAVMVMALLAVVGLFTTVVRHDA  
ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**  
 GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTAAGTCTGAGTCCTGGGGACATTTCGATACA  
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGG**TAGA**AAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
 GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

1003530.121204  
 1003530.121204

## FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
```

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIH DYLYFQVLS PGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQE HGGRAVIIISDNAVDNDSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGTGGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATAACATTGTATGGAT  
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGAA**TAA**AAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE
```

### Important features of the protein:

Signal peptide:

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

## Phospholipase A2 histidine active site.

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGGCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAAC TCACCCGTGGGTCGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

**FIGURE 224**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
```

```
><subunit 1 of 1, 178 aa, 1 stop
```

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK

LGDSWDVKLGALGGNTQEVTLPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

GCTGTAGCGTGTGTCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGACGCTCTGTGGCT  
 GAACTGGGTGCTCATCACGGGAAGTCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTC  
 ACAGGGGCTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGG**ATC**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAAAGTAAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGBAAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAAGTTTACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTCTAG  
 GACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTTTCAGTGGACCCAGTGTTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTG  
 AAAAGTTTTAAAGGTCTAAGGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTTGAGGTA  
**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAAGTC  
 TGGTGACTATCAAGGGAACGCGATGCCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG  
 CAAGATCCTTCCTTGTCCGTTTTAGTGCATTCATAATACTGGTCATTTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGTCCGGTTTTAATATAA  
 TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTTGTTTTAAGATAAAAGT  
 TCTTTTCATAGGTAAAAA



**FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301  
><subunit 1 of 1, 513 aa, 1 stop  
><MW: 58266, pI: 9.84, NX(S/T): 4  
MGFNVIRLLSGSAVALVIAPT VLLTMLS SAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG  
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF  
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL  
DLGYNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTM  
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLA  
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA  
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI  
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMT PSTQEFYVDYKPTNTETSEM LLN  
GTGPCTYNKSGSRECEV

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
 TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
 TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG  
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
 TTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAACTCTTTC  
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAPAGGAAAAGATTACAAGTCT  
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG  
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
 AAACATCAATAGATATCTAAAAA

**FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

10015610123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

**FIGURE 229**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAAACT  
 CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTCAAGTCTTGATTTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGCTTCTTCAGAA**ATG**TTTTTTA  
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT  
 TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGAT**TAG**CAGTTGAAAATCACCTTGTC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC  
 TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG  
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCAATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTTATGATGAGAGTAACAATA  
 AAGTATTCATGATTTTTTCACATACATGAATGTTTCATTTAAAAGTTTAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTTGTGCTGCATTAAATTTGCTTGGAAGTGTTAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAATAAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCACAGGGAACCCTAATCTTGGGTAAATCTAGTATAAAACAAATTATACTTTTAT  
 TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTCATAGTATTTATT  
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
 TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTTCTCTTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

**FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
```

```
><subunit 1 of 1, 140 aa, 1 stop
```

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL  
VPVTTNKRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT  
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG  
GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA  
CTTGGACCTGTCCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCGGGGCT  
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTACTGCC  
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG  
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
CACAACCTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCACCAT  
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG  
CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCCAG  
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGGACCTGTCGGGCAACCCCAAGCTTAAC  
GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
AACCTGGTGCCCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT  
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  
ATCTT**TGA**CAAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCTCTGGGCTGCCTCAG  
GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCAAGTGGGGAGCCCGCAGGCCTATGTGGCA  
GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCTTCCCTCAT  
GCCTGGGCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
GTTCAGGTCCACTGGGCTGAGTGTCCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT  
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCCGCTTCATCCTTTTCTAT  
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC  
AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCCGACCCAATGCACTTTCTTGTCTCCTCTA  
ATAAGCCCCACCCTCCCCGCCTGGGCTCCCCCTGCTGCCCTTGCTGTTCCCCATTAGCACA  
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
CCAGCCTAGCCAGTTTCTCACCCCTGGGTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC  
CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
TCTGGCTGGGATCTCCAAGGGCCTCCTGGATTAGTCCCCACTGGCCCTGAGCACGACAGC  
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC  
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTTAGTCTTCATTTTA  
TAAAAGTTGTTGCCTTTTTAACGGAGTGTCACCTTTCAACCGGCCTCCCCTACCCCTGCTGGC  
CGGGGATGGAGACATGTCATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAAT  
ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC  
CCATCATCTATCTAACCGGTCTTGATTTAATAAACACTATAAAAGGTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLEVSVSFAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS  
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSLQELDLSGTNLVPLPEALLLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
 AAACAAGTTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAATATCTT  
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT  
 ATTTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTTTATACAGTAAAAAATAACCTTGTAATTCTAGAAGAGTGCT  
 AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAAAAA



**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPEMSFSIYSLQVPAVPGGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCG  
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA  
GCCCTAGGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTTATTGGCCAGTTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAAGATGCAAAT  
GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTCGCGATTTTCGTGGTGTACATCATGCATTTG  
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGT  
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTT**TAA**

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568  
><subunit 1 of 1, 323 aa, 1 stop  
><MW: 36064, pI: 9.33, NX(S/T): 1  
MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH  
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGKPLRFRGVHHAFKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAA**ATC**GCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTTCATGTTGATGTTTGGGTCACCTATTGCTTCCATGTGGATTCTTTTTTGGTGC  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA  
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCT**GA**GATCAC  
TTCTTAAGTCACATTTTCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTTATGTTT  
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTTAGAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAAGGTTTTAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA  
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC  
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

10056012001

**FIGURE 239**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
 GGTGAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  
**GATG**AGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTATTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
 AGCCAACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGTGCACTGGTGCTGGTGG  
 CCTCCTACGACGATCCAGGGACCAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG  
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTT**TAG**GGTGGC  
 TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCCG  
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGACGC  
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG  
 ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
 TTTTGTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSFMSKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

FOOTNOTES

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCTAGTCCTCTAGTCCTCAAATTTCCAGTCCC  
 CTGCACCCCTTCCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC  
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA  
 GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
 CTTTGGACCTGCACAACAATGGCCACACAGTGAACCTCTCTCTGCCCTCTACCCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
 CCTTCTCCTGGCTGTTTTATTTTCAATTGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCA  
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAAGTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG  
 GAAGTTTGGGATATACCCCAAAGTCTTACCCCTCACTTTTATGGCCCTTTCCCTAGATA  
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA  
 TATTTGGAAATTAAAGTTTCTGACTTT



**FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812  
><subunit 1 of 1, 337 aa, 1 stop  
><MW: 37668, pI: 6.27, NX(S/T): 1  
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ  
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT  
FSTEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 243**

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC  
GTGGACCCAAAGGTAGCAATCTGAAAC**ATG**AGGAGTACGATTCTACTGTTTTGTCTTCTAGG  
ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC  
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG  
ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG  
AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC  
TGCACCCACATGTGTTACCAATTTTTGTGCACACAACCTTGGAGCCCAGGGCACTATCCTAAGC  
TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCAT  
CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG  
GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCGCCTCCCAACTCCCAGTGGC  
ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA  
GGAAGCCACCACAGAATCAGCAAATGGAATTCAG**TAA**GCTGTTTCAAATTTTTTCAACTAAG  
CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA  
GACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATTTACCTGAAAATATTCTTGAAATT  
TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT  
CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAAACATATTTGGAAA  
ACTGGAAA  
AAAAAAAAAAAAAAAAAAAAA

T00560:246

## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHHPVLPPIFVTQLGAQGTLISSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

Downloaded from www.jstor.org

**FIGURE 245**

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
 GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCG  
 GCAGCCGGGAGCC**ATG**CGACCCCAAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCC  
 TGCTGCTCCTGCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG  
 GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
 AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
 CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA  
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**  
**A**ATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT  
 GGTTTCAATATTTTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
 TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
 TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT  
 AAAAATTATTTCCAACA

30015610 "424501  
 30015610 "424501

**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

1050-2000